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191509

From: Hamud, Fozia
Sent: Wednesday, May 31, 2006 1:28 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 10/732,796

URFB

Kindly search SEQ ID NOs: 11 and 12 of 10/732,796 against commercial and interference data bases. thank you.

FOZIA HAMUD
PATENT EXAMINER
ART UNIT 1647
ROOM: REM 4D64
MAIL BOX: REM 4C70

Noted

Searcher: _____
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Date Searcher Picked up: _____
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Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
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WWW/Internet: _____
Other (Specify): _____

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OM protein - protein search, using sw model

Run on: June 2, 2006, 22:53:51 ; Search time 52 Seconds
(without alignments)
1339.892 Million cell updates/sec

Title: US-10-732-796a-12

Perfect score: 4154

Sequence: 1 MTKDEPIVKSHPVCLMII.....IRAFNMKLTIVENNVDYS 796

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
1: /EMC Celerra_SIDS3/ptodata/2/1aa/5_COMB.pep:*
2: /EMC Celerra_SIDS3/ptodata/2/1aa/6_COMB.pep:*
3: /EMC Celerra_SIDS3/ptodata/2/1aa/7_COMB.pep:*
4: /EMC Celerra_SIDS3/ptodata/2/1aa/H_COMB.pep:*
5: /EMC Celerra_SIDS3/ptodata/2/1aa/PTUS_COMB.pep:*
6: /EMC Celerra_SIDS3/ptodata/2/1aa/RE_COMB.pep:*
7: /EMC Celerra_SIDS3/ptodata/2/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4154	100.0	802	US-09-949-002-512	Sequence 512, App
2	4149	99.9	796	US-09-949-002-386	Sequence 386, App
3	2830	68.1	786	US-09-949-002-351	Sequence 351, App
4	2459	59.2	672	US-09-949-002-522	Sequence 522, App
5	1905.5	45.9	811	US-09-991-181-57	Sequence 57, App
6	1905.5	45.9	811	US-09-990-444-57	Sequence 57, App
7	1905.5	45.9	811	US-09-997-333-57	Sequence 57, App
8	1905.5	45.9	811	US-09-992-598-57	Sequence 57, App
9	1905.5	45.9	811	US-09-989-735-57	Sequence 57, App
10	1905.5	45.9	811	US-09-989-726-57	Sequence 57, App
11	1905.5	45.9	811	US-09-997-514-57	Sequence 57, App
12	1905.5	45.9	811	US-09-989-728-57	Sequence 57, App
13	1905.5	45.9	811	US-09-997-349-57	Sequence 57, App
14	1905.5	45.9	811	US-09-997-653-57	Sequence 57, App
15	1905.5	45.9	811	US-09-989-293A-57	Sequence 57, App
16	940	22.6	784	US-09-982-308B-23	Sequence 23, App
17	837	20.1	775	US-09-949-016-8799	Sequence 8799, App
18	504	12.1	739	US-09-396-985B-4	Sequence 4, App
19	504	12.1	839	US-09-396-985B-2	Sequence 2, App
20	504	12.1	839	US-09-396-985B-98	Sequence 98, App
21	504	12.1	844	US-09-949-016-9438	Sequence 9438, App
22	496	11.9	1059	US-09-954-987B-187	Sequence 187, App
23	488.5	11.8	1041	US-09-999-833A-498	Sequence 498, App
24	488.5	11.8	1041	US-09-954-987B-184	Sequence 184, App
25	488.5	11.8	1041	US-09-954-987B-186	Sequence 186, App
26	488.5	11.8	1041	US-10-020-445A-498	Sequence 498, App

27	488.5	11.8	1041	2	US-09-978-189-498	Sequence 498, App
28	488.5	11.8	1041	2	US-10-017-085A-498	Sequence 498, App
29	488.5	11.8	1041	3	US-10-145-129A-498	Sequence 498, App
30	488.5	11.8	1041	3	US-10-013-929A-498	Sequence 498, App
31	488.5	11.8	1041	3	US-10-013-917A-498	Sequence 498, App
32	481.5	11.6	904	2	US-09-949-002-352	Sequence 352, App
33	481.5	11.6	910	2	US-09-949-002-483	Sequence 483, App
34	449.5	10.8	1049	2	US-09-954-987B-172	Sequence 172, App
35	446.5	10.7	1049	2	US-09-999-833A-496	Sequence 496, App
36	446.5	10.7	1049	2	US-09-954-987B-170	Sequence 170, App
37	446.5	10.7	1049	2	US-10-020-445A-496	Sequence 496, App
38	446.5	10.7	1049	2	US-09-978-189-496	Sequence 496, App
39	446.5	10.7	1049	2	US-10-017-085A-496	Sequence 496, App
40	446.5	10.7	1049	3	US-10-145-129A-496	Sequence 496, App
41	446.5	10.7	1049	3	US-10-013-929A-496	Sequence 496, App
42	446.5	10.7	1049	3	US-10-013-917A-496	Sequence 496, App
43	444.5	10.7	989	2	US-09-954-987B-175	Sequence 175, App
44	444.5	10.7	989	2	US-09-954-987B-171	Sequence 171, App
45	441.5	10.6	835	3	US-09-396-985B-6	Sequence 6, App

ALIGNMENTS

RESULT 1	US-09-949-002-512	Application US/09949002
Sequence 512, Application	US/09949002	
Patent No. 6900016		
GENERAL INFORMATION:		
APPLICANT: VENTER, J. Craig et al.		
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION		
TITLE OF INVENTION: AND USES THEREOF		
FILE REFERENCE: CL000790		
CURRENT APPLICATION NUMBER: US/09/949,002		
CURRENT FILING DATE: 2000-01-28		
PRIOR APPLICATION NUMBER: 60/231,401		
PRIOR FILING DATE: 2000-09-08		
NUMBER OF SEQ ID NOS: 10823		
SOFTWARE: FASTSEQ for Windows Version 4.0		
SEQ ID NO 512		
LENGTH: 802		
TYPE: PRT		
ORGANISM: Human		
US-09-949-002-512		
Query Match	100.0%; Score 4154; DB 2; Length 802;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 796; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MTKDEPIVKSHPVCLMIIIVGTRIQPSDGNFPAVDSKRGILHVPKDLPLTKVLNDS 60	
DB	7 MTKDEPIVKSHPVCLMIIIVGTRIQPSDGNFPAVDSKRGILHVPKDLPLTKVLNDS 66	
QY	61 QNYIAYELQVSDSPFSELTIVLRISNRRIQDLISVFKFQDDELYDLSNOLQKISCHPI 120	
DB	67 QNYIAYELQVSDSPFSELTIVLRISNRRIQDLISVFKFQDDELYDLSNOLQKISCHPI 126	
QY	121 VSEFRHLDSFNDPKALPICKERGNLSQNLFLGLSAMKQKDLPLFAHLHLSYIILDLRN 180	
DB	127 VSEFRHLDSFNDPKALPICKERGNLSQNLFLGLSAMKQKDLPLFAHLHLSYIILDLRN 186	
QY	181 YIKENEFESLOILNAKTLHLVFPHTSLPAIVNISVNTLGLQLTNKLNDNCQVFLK 240	
DB	187 YIKENEFESLOILNAKTLHLVFPHTSLPAIVNISVNTLGLQLTNKLNDNCQVFLK 246	
QY	241 FLSSELTTRGSLNFTLNHIETTKCLVRFQFLMPKPEYVANIYNLTIIESIREEDFTYS 300	
DB	247 FLSSELTTRGSLNFTLNHIETTKCLVRFQFLMPKPEYVANIYNLTIIESIREEDFTYS 306	
QY	301 KTKLKALTIETHTNOVFLFSQALATYVPSNNIMMLTISDTPFIHMLCPHAPSTFKFLNF 360	
DB	307 KTKLKALTIETHTNOVFLFSQALATYVPSNNIMMLTISDTPFIHMLCPHAPSTFKFLNF 366	

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QY 361 TONVFTDSIFEKCSFLVLETLIIQKNGKDLFKVGLMTKOMPSEIIDVSNLSGSRH 420
Db 367 TONVFTDSIFEKCSFLVLETLIIQKNGKDLFKVGLMTKOMPSEIIDVSNLSGSRH 426
QY 421 KENCWVSIIVNLSSNMULTSVRCPLPRRIKVDHNSNKIKSVPKQVVKLEALQELNV 480
Db 427 KENCWVSIIVNLSSNMULTSVRCPLPRRIKVDHNSNKIKSVPKQVVKLEALQELNV 486
QY 481 AFNSLTDLPGCGSFSSLSVLIIIDHNSVSHPSADPFQSCQKRSIRAGDNPCCTCELREF 540
Db 487 AFNSLTDLPGCGSFSSLSVLIIIDHNSVSHPSADPFQSCQKRSIRAGDNPCCTCELREF 546
QY 541 VKNIDVSEVLEGPDSYKCDYPESYRGSPLKDFHMSLSCNTLLIITGATMLVLAV 600
Db 547 VKNIDVSEVLEGPDSYKCDYPESYRGSPLKDFHMSLSCNTLLIITGATMLVLAV 606
QY 601 TVTSLCIYLDLPWYIRMCQWOTQRRRANIPLEBELQNLQFHAFISYSEHDSAMVKSSEL 660
Db 607 TVTSLCIYLDLPWYIRMCQWOTQRRRANIPLEBELQNLQFHAFISYSEHDSAMVKSSEL 666
QY 661 VPLYEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSI FVLSPNFVQSEWCHYELYPAH 720
Db 667 VPLYEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSI FVLSPNFVQSEWCHYELYPAH 726
QY 721 HNLFHGSGNNLILILEPIPNKYNKHLKALMTORTYLOMPKESKRGFLFMANIRAA 780
Db 727 HNLFHGSGNNLILILEPIPNKYNKHLKALMTORTYLOMPKESKRGFLFMANIRAA 786
QY 781 FNMKLTIVTENNDVKS 796
Db 787 FNMKLTIVTENNDVKS 802
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RESULT 2
US-09-949-002-386
; Sequence 386, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: AND USES THEREOF
; FILE REFERENCE: CLO00790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 386
; LENGTH: 796
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-386
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Query Match 99.9%; Score 4149; DB 2; Length 796;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MTOKKEPIVKSFFHVCMLIIIVGTRIQFSDGNEFAVDKSKRGLIHVPKDPLKTKYLDMS 60
Db 1 MTOKKEPIVKSFFHVCMLIIIVGTRIQFSDGNEFAVDKSKRGLIHVPKDPLKTKYLDMS 60
QY 61 QNYIAELQVSDMSFSELTVLRLSHNRIOQLDLVSFKFQODLEAYDLSNQOKISCHPI 120
Db 61 QNYIAELQVSDMSFSELTVLRLSHNRIOQLDLVSFKFQODLEAYDLSNQOKISCHPI 120
QY 121 VSFRLHDSFNDFKALPICKEFGNLSQNLFLGISAAMKLOKDLPLPAHHLIYIILDLRN 180
Db 121 VSFRLHDSFNDFKALPICKEFGNLSQNLFLGISAAMKLOKDLPLPAHHLIYIILDLRN 180
QY 181 YYIKENETESIQLINAKTLHLVFPHTSLFAIQVNISVNTLGGCLQTLNIKLNDNCQVFIK 240
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Db 181 YYIKENETESIQLINAKTLHLVFPHTSLFAIQVNISVNTLGGCLQTLNIKLNDNCQVFIK 240
QY 241 FLSLETRGSTLNFNTLNIETTWKCLVAVFOFLMPKPEYININYLATIIIESIREDDFTYS 300
Db 241 FLSLETRGSTLNFNTLNIETTWKCLVAVFOFLMPKPEYININYLATIIIESIREDDFTYS 300
QY 301 KTTLKALTIIEHTNOVPLFSQALYTVFSEKNIIMMLTISDTPFIHMLCPHAPSTKPLNF 360
Db 301 KTTLKALTIIEHTNOVPLFSQALYTVFSEKNIIMMLTISDTPFIHMLCPHAPSTKPLNF 360
QY 361 TONVFTDSIFEKCSFLVLETLIIQKNGKDLFKVGLMTKOMPSEIIDVSNLSGSRH 420
Db 367 TONVFTDSIFEKCSFLVLETLIIQKNGKDLFKVGLMTKOMPSEIIDVSNLSGSRH 426
QY 421 KENCWVSIIVNLSSNMULTSVRCPLPRRIKVDHNSNKIKSVPKQVVKLEALQELNV 480
Db 427 KENCWVSIIVNLSSNMULTSVRCPLPRRIKVDHNSNKIKSVPKQVVKLEALQELNV 486
QY 481 AFNSLTDLPGCGSFSSLSVLIIIDHNSVSHPSADPFQSCQKRSIRAGDNPCCTCELREF 540
Db 487 AFNSLTDLPGCGSFSSLSVLIIIDHNSVSHPSADPFQSCQKRSIRAGDNPCCTCELREF 546
QY 541 VKNIDVSEVLEGPDSYKCDYPESYRGSPLKDFHMSLSCNTLLIITGATMLVLAV 600
Db 547 VKNIDVSEVLEGPDSYKCDYPESYRGSPLKDFHMSLSCNTLLIITGATMLVLAV 606
QY 601 TVTSLCIYLDLPWYIRMCQWOTQRRRANIPLEBELQNLQFHAFISYSEHDSAMVKSSEL 660
Db 607 TVTSLCIYLDLPWYIRMCQWOTQRRRANIPLEBELQNLQFHAFISYSEHDSAMVKSSEL 666
QY 661 VPLYEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSI FVLSPNFVQSEWCHYELYPAH 720
Db 667 VPLYEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSI FVLSPNFVQSEWCHYELYPAH 726
QY 721 HNLFHGSGNNLILILEPIPNKYNKHLKALMTORTYLOMPKESKRGFLFMANIRAA 780
Db 727 HNLFHGSGNNLILILEPIPNKYNKHLKALMTORTYLOMPKESKRGFLFMANIRAA 786
QY 781 FNMKLTIVTENNDVKS 796
Db 787 FNMKLTIVTENNDVKS 802
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RESULT 3
US-09-949-002-351
; Sequence 351, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: AND USES THEREOF
; FILE REFERENCE: CLO00790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 351
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-351
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Query Match 68.1%; Score 2830; DB 2; Length 786;
Best Local Similarity 69.5%; Pred. No. 1e-262;
Matches 540; Conservative 92; Mismatches 143; Indels 2; Gaps 1;
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QY 12 FHFVCLMIIIVGTRIQFSDGNEFAVDKSKRGLIHVPKDPLKTKYLDMSQNYIAELQVSD 71
Db 5 FHFVCLMIIIVGTRIQFSDGNEFAVDKSKRGLIHVPKDPLKTKYLDMSQNYIAELQVSD 64
```


/ APPLICANT: Paoni, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Watanabe, Colin K.
 / APPLICANT: Williams, P. Mickey
 / APPLICANT: Wood, William I.
 / APPLICANT: Zhang, Zemin
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 / FILE REFERENCE: P2730PIC53
 / CURRENT FILING DATE: 2001-11-16
 / PRIOR APPLICATION NUMBER: 60/049787
 / PRIOR FILING DATE: 1997-06-16
 / PRIOR APPLICATION NUMBER: 60/062250
 / PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 45.9%; Score 1905.5; DB 2; Length 811;

Beet Local Similarity 47.8%; Pred. No. 8,2e-174; Matches 382; Conservative 145; Mismatches 251; Indels 21; Gaps 10;

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QY 8 IVKSFHFVCLMTIIV-GTRIQFSDGNEFAVDKSKRGLIHVPKDLPLKTKVLMSQNYIAE 66
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DB 3 LIRNIYIFGSIWMTAGDAPELPEERELMTNCSNMSLRVPADLPATTTLDLSVYLQ 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 LOVDSMFSLELTVLRLSHNRITQLDLSVFKENODLEYLDLSHNOLOKISCHPIYSFRLL 126
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DB 63 IQSSDFHSVSKRLVLLCHNRIOQLDLKTFEENKEIRYIDLNNRLKSVTWYLLAGRLYL 122
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QY 127 DISFDFKALPICKEKGNSQLNPLGLSAMKLOKLDLPIAHHLISYLLDLRNYIKEN 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 123 DISFDFDMPICEEAGNMSHLEIIGLSAKIQKSDFOKIAHLNLTAVLGFRT--LPHY 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 187 ETESQILNAKTLHVFHPTSLFAIQVNISVNTLGLQTLNKLNDNCQVFIKFLSELT 246
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DB 181 EEGSIPILNTTKTLHVLPMDFWILRRGITSKILMTNT----DGKSQVSY--ENQ 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 247 RGSSTLN----FTLNHETWKCIVRFQFLMPKPREVLYNTLT--IESIREDFPY 299
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DB 245 RMLSENAKTSVLLINKVDLLMDDLFLLIQFVWHTSVEHFQIRNVTFGKAYLDHNSFDY 294
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QY 300 SKTTLKALHIEHTNOVFLFSQALYTVFSENNIMMLTSDPRFTIMLCPHAPSTFKEN 359
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DB 295 SNTVKTITLHVFHPTSLFAIQVNISVNTLGLQTLNKLNDNCQVFIKFLSELT 354
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QY 360 FTQNVFTSIFEKSCSTLVLETLIILOKNGIKDLFKVGLMTKMPSELEILDVSNLSER 419
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QY 420 KHEKCTWASIVVNLSSNMLTDSVPRCLPPRAKVLIDLHNSIKSVKQVYKLEALQELN 479
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DB 413 NDENCSWPEVTVNMNLSYKRLSDSVPRCLPKSIQIIDLNNNOIQVPEKTIHLMALREIN 472
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DB 473 IAFNFLTDLPGCSHRSRLSVLNIEMNFIISPGLDFVQSCQEVXYTLNAGNPPRCCTELKN 532
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QY 540 EYKNIIDQVSSEVLEGMPSDKCDYPBSYRGSGLKPFHMSLSNTLLVTTGATMLVLA 599
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DB 533 FIO-LETYSVWVWVMSDSYCEPYLNLGRTRLKDVHHELSCTALLIVTIVMLVVG 591
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 600 VVVTSLCTIYLDLPMYLRMVCQWTOFRRARANIPLERLONLQFHAISYSEHSDSAVKS 659
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DB 592 LVAFPCCLHFDLPWYLRMLGQCTQWHRVRKTTQEOLEKSNVRPHAFISYSEHSDLVKN 651
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QY 660 LVPLYLEKED--IOICLHERNFVPGKSIYENIINCIEKSYKSIFFVLSPNFQSEWCHYEY 717
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 652 LIPNLEKEDGSLICLYESYFPDGKSIENIYVFIKSYKSIFFVLSPNFQSEWCHYEY 711
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 718 FAHNLPHGSGNNLILILEPIQNSIPNKYHKLKALMTQRTYLLQMPKEKSRGLFWANI 777
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 712 FAHNLPHGSGNNLILILEPIQNSIPNKYHKLKALMTQRTYLLQMPKEKSRGLFWANI 771
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 778 RAAFNMKLTLYENNDVKS 796
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DB 772 RAINVNVLATREMYELOQT 790
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RESULT 6
US-09-990-444-57
; Sequence 57, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC19
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322

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[illegible]

; PRIOR FILING DATE: 1998-07-02
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 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match	45.9%;	Score 1905.5;	DB 2;	Length 811;
Best Local Similarity	47.8%;	Pred. No. 8.2e-174;		
Matches 382;	Conservative 145;	Mismatches 251;	Indels 21;	Gaps 10;

Qy	8	IVKSHFPCMI IIV-GTROIQSDGNEFAVDSKRGELIHPKOLPKTKYLDMSOVIAE	66
Dz	3	LIRNIYICSIYMTAGDAPBELPERBELMTNCSNMSLRKVPADULTPATITLIDLSYMLDFO	62
Qy	67	LQVSDMSFLSELTVLRLSHNRIOQLDLVSFKPNODLEYLDLSHNOLOKISCHDVSFRIL	126
Dz	63	LQSSDFHVSFKRLRYILCHNRIOQLDLKFFEEFKELRYLDLSNNRKSVYWMYLAGRLYL	122
Qy	127	DLSPNDFKALPCKEFCNLSQANFLGLSAMKQOKDLDLPIAHNLSTYLLDLNRYIKEN	186
Dz	123	DLSPNDFKALPCKEFCNLSQANFLGLSAMKQOKDLDLPIAHNLSTYLLDLNRYIKEN	186
Qy	187	ETESHOINAKTLIVHPHTSLFAIOVNI SVNTLGLQLOTNIKYANDNCQVFKFPISELT	246
Dz	181	BEGSPLINTYKGLIHLPMDTNFWMLRGITKSKLEMTNI---DGKSQVSY--EMQ 234	
Qy	247	RGSITLLN-----FTLNHLETTWKCLVRVQFQFMPKPEVEYALINYULTI--IESIREDEFTY	239
Dz	235	RNLSENAKTSVILNNKVDLLMDWDLFLIQFWHTSVEHFQIRNVTFGKAYLDHNSFDY	294
Qy	300	SKTLIKALTIETHTNOVLFQSGTALYTVSENNIMULTISDPRFIMLCPHASTKFLN	359
Dz	295	SNVTWRITKLEHVRVFYIOODKIYLLTKMDIENLTISNAQMPHMLPPNPTKQOYLX	354
Qy	360	FTONVFTSIEFKGCTVKELETLIOKNGKXOLFVKYGLMTKMPKSEIILDVSNNSIESGR	419
Dz	355	PANNILDBELKRTIQLPHLKTILANGKLETLISVSCFANNTP-LEHDLSONLLQH-K 412	
Qy	420	HKENCWTVESIVLNLSSNMLTDSVFRCLPRIKVYLDHSHNKIKSVKQVVKLEALOELN	479
Dz	413	NDENCSWPEYVNNMLSYNKLSDSVFRCLPKSIOQLDLNNOQIOTVPKETIHLMLREIN	472
Qy	480	VAFNSITLDBCCGSSSLSYLIDHNSVSHBPADFPQSOQRKSTAKGDNPPCTCELE	539
Dz	473	IAFNFLTDLPCGSHFSRLSVLNIENNFIILSPBLDFVQSOQEVKXTLAGNPPRCTCELE	532
Qy	540	FVKNIQVSSSEVLLEGMPDSYKCDYPSRYGSEPLKDFHMSSELCNITLLIVTIGATMYLYA	599
Dz	533	FIQ-LETTYSEVMWVMMSDSTCYEYPLNRGRTGLKDYHLELSCNTALLIVTIVIMLYA	591
Qy	600	VTVTSLCITLDDLFWYLRVQCMQOTRRRARNIPLBELQNLQFHAETISYSEHDSAWKSE	659
Dz	592	LAVAFCCCHPDLFWYLRVQCMQOTRRRARNIPLBELQNLQFHAETISYSEHDSAWKSE	651
Qy	660	LVPFLKED--IQTLHERNFPYRGSIYENIINCIEFKSKSI FVLSPNVQSWCHYEYEL	717
Dz	652	LIPNLEKDGSLICLYESYDFPGKSISENIYSFIEKSKSIFVLSPNVQSWCHYEYEL	711
Qy	718	FAHNHLFREGSNLLILLEPIPONSIPKRYKLLKALMTQRYTLOQPEKSKRGLEFWANI	777
Dz	712	FAHNHLFRENHDHILILEPIPFYCIPIRYNKLKALLEKAYLEMPKRRKCGLEFWANI	771
Qy	778	RAARNKTLTYTENNDAVS 796	
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RESULT 7
US-09-997-333-57
; Sequence 57, Application US/09997333
; Patent No. 6953836

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Geriltsen, Mary E.

APPLICANT: Goddard, Audrey

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APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

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APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Matanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P2730P1C27

CURRENT APPLICATION NUMBER: US/09/997,333

CURRENT FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 45.9%; Score 1905.5; DB 2; Length 811;
Best Local Similarity 47.8%; Fred. No. 8.2e-174; Indels 21; Gaps 10;
Matches 382; Conservative 145; Mismatches 251;

QY 8 IYKSFHFCVCMITIIY-GTRIOFSDNEPAVVKSKXGLIHPKDLPLKTKVLDMSQNTYAE 66
DB 3 LIRNIYIFCSIVMTAKGAPLPEREREIMTCSNMSLRKRVADLPATTTDLSINLLFQ 62
QY 67 LQVSDMSFLSELTVLRLSHNRIOULDLSVFXFNODLEYLDLSHNOLOKISCHPIVSFRL 126
DB 63 LQSDSFHVSVKLRVYLILCHNRIOQLDLDKTFEFNKELRYLDLSNNRKLKSVYLLAGRLYL 122
QY 127 DISFNDPKALPICKFEGULSQNLFIGLSAMKLOKLDLPIAHLSYLLDLRNYIKEN 186
DB 123 DLSFNDPFTMPICEAGNMSHLEILGSGAKIOKSDFOKIALHINTVFLGERT--LPHY 180
QY 187 ETESQIINAKTILHVFHPTSLEAIVQNISVNTLGLQLOTVNIKUNDNCQVFIKFLSELT 246
DB 181 BEGSLPIINTTKLHVLPMDTNFWVLKRDGIKTISKILEKMTNI---DKSQSFVSY--EMQ 234

QY 247 GGSSTLNN-----FTLNHETWKKLVAVQOFLPKRPVEYANINLNT--IESI-REEDFTY 299
 Db 225 RNLSTENATSVLLNKVLLMDDELLIIOFVHTSVEHQIKNNVITGGCAIYLDHNSFDY 294
 QY 300 SKTTLKALTLTEHTNQVFLPFSQATLVTVSENNIMMLTISDPFIHMLCEHASTPEKFLN 359
 Db 225 SNTVWRTIKLEHVHPRVFYIQODKIKYLLLTKMDIENULTISNAQMPHLPFNYPFTKPYLN 354
 QY 360 FFGQNVFTDSIFPEKCSGLVLEETLILOKNGKLDFKVGKMTKMPSLBILDVSNNSLESGR 419
 Db 355 FANNILITDELFRKTIQPLPHLKTLLINGNKLETLSVSCFANNTP-LEHLDLSQNLLOH-K 412
 QY 420 HKNENTWVESIVVNLSSMMLTDSVPRCLPRLKVLDSHNKIKSVPKQVVKLEALOELN 479
 Db 413 NDENCSWPEVTVNNMLSYNKLSDSVPRCLPKSIQIIDLNNQIOTVPEKETHLMALRELN 472
 QY 480 VAFNSGLTDLPGGCSFSSLSVLLIIDHNSVSHPSADFPQSCOKMSIRAGNDPFOCTCELR 539
 Db 413 IAFNFLTDLPGCSHPSRLSVLNIENMFILSPSLDFQSCQEVVTLIAGNRPFCCTCEKN 532
 QY 540 FVKNIQDVSSSEVLGMPDSYKCDYPESYRGSPLKDFHMSLSGNTLLIIVTIGATMLVLA 599
 Db 533 FIO-Q-LETYSEVMMVGMDSYTCBYPNLNKGTRKLDVHLBELSNTALLIYIVIMVLG 591
 QY 600 VTVTSLCIYLDLPWYIRMYCOMTQTRRRANPLPELQORLQLOHAFISYSEHSANWYKS 659
 Db 592 LAVAPCCAHFDLPWYIRMYGQCTQTHRRVAKTQEOELKNVRPHAFISYSEHSLWYKNE 651
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 Db 652 LIPNLEKEGSLILICYESYFDPBGKSIENIVSIFIKSYKSIIVLSPNFQONWCHIEFY 711
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 Db 712 FAHNHLFHEHNSDHIILILEPIFYCIPRYHKLKALLEKAYLEWPKDRKCGFLPWANL 771
 QY 778 RAAPFMKLTIVENNVDYS 796
 Db 772 RAAINVNLATREMYELQT 790
 RESULT 8
 US-09-992-598-57
 / Sequence 57, Application US/09992598
 / Patent No. 6956108
 / GENERAL INFORMATION:
 / APPLICANT: Ashkenazi, Avi J.
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan L.
 / APPLICANT: Ferrara, Napoleone
 / APPLICANT: Fong, Sherman
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 / APPLICANT: Gerritsen, Mary E.
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 / APPLICANT: Kijavlin, Ivar J.
 / APPLICANT: Napier, Mary A.
 / APPLICANT: Pan, James
 / APPLICANT: Paoni, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Watanabe, Colin K.
 / APPLICANT: Williams, P. Mickey
 / APPLICANT: Wood, William I.
 / APPLICANT: Zhang, Zemin
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 / TITLE REFERENCE: P2730PIC20

1	CURRENT APPLICATION NUMBER: US/09/992,558
2	CURRENT FILING DATE: 2001-11-14
3	PRIOR APPLICATION NUMBER: 60/049787
4	PRIOR FILING DATE: 1997-06-16
5	PRIOR APPLICATION NUMBER: 60/062250
6	PRIOR FILING DATE: 1997-10-17
7	PRIOR APPLICATION NUMBER: 60/065186
8	PRIOR FILING DATE: 1997-11-12
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10	PRIOR FILING DATE: 1997-11-13
11	PRIOR APPLICATION NUMBER: 60/066770
12	PRIOR FILING DATE: 1997-11-24
13	PRIOR APPLICATION NUMBER: 60/075545
14	PRIOR FILING DATE: 1998-02-25
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16	PRIOR FILING DATE: 1998-03-20
17	PRIOR APPLICATION NUMBER: 60/083322
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19	PRIOR APPLICATION NUMBER: 60/084600
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66	PRIOR FILING DATE: 1998-06-11
67	PRIOR APPLICATION NUMBER: 60/088861
68	PRIOR FILING DATE: 1998-06-11
69	PRIOR APPLICATION NUMBER: 60/088876

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC60
CURRENT FILING DATE: 2001-11-19
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      45.9%; Score 1905.5; DB 3; Length 811;
Best Local Similarity 47.8%; Pred. No. 8.2e-174;
Matches 382; Conservative 145; Mismatches 251; Indels 21; Gaps 10;

QY      8 IVKSHFPCMIITV-GRRIOFSDGNEPVDKSKGLIHVPDLPKTKVLMSONYIAE 66
      3 LIRNIYIFCSIVMTAEGDAPELPERERELMTNCSNMSLRKVPADLPATTTLDLSTNLLFQ 62
      67 LQVSMFSFSELTVALSHNRIOQLDLVFKFNQDLEVLDLSHNOLOKISCHPIVSFRHL 126
      63 LQSSPFHSVSKIRVLILCHNRIOQLDLKTFEENKEIRYLDLSNNRKSTVWLLAGRLV 122
QY      127 DLSFNDPKALPICKEFGNISQNLPIGLSAMKLOKLDLPDAHLSYILLDIRNYIKEN 186
      123 DLSFNDPFTMPICEBAGNMSHLEILGLSGAKIOKSDFOKIAHLHNTAVFLGERT--LPHY 180
QY      187 ETESQIINAKTLHIVFHTSLFALQOVNISVNTLGLQLOLTINKANDNOQVITIKFSELT 246
      181 EEGSLPIINTYTKLHIVLPMNDINFWLIRGDKITSKILEMTNI---DGKSQFVSY--EMQ 234
QY      247 RGSSTLNL-----FTLNHLETTWKCLVRVPOFLMPKREVEYLNINYLTI--IESIREEDFY 299
      235 RNLSLSENAKTSVLNKLVDLMDLLEFLIIQFVWHISVEHFQIRNRYFGGKALIDHNSFY 294
Db      295 SNTVAKTKLEHVHRVFYIQODKIYLLTKMDIENLITSNQOMPMLFPNYPTKFOYLN 354
QY      300 SKTTIKALTIETITNOVLFSSQATAYTVESENNIMLTTISDPPFIHMLCPHAPSTFKFLN 359
      360 FTQNVFTDISIFPKSGTVLVLETLILQXNGLKDLFKYGLMTXKMPSEILIDVSWNSLESOR 419
      355 FANNITLDELFRRTIQLPHLKTLILNGNLETLTSLVSCFANNTP--LEHLDLSQNLLOH-K 412
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QY      420 HKNCTWVESIVVLNLSNNMLTDSVFRCLPPRIKVLIDLHSNKIKSVKQVVKLEALOELN 479
      413 NDENCSWPEETVANNMLSYNKLSDSVFRCLPKSIOQLDLANNQIOVPEKETHLMALRELN 472
QY      480 VAFNSLTLDPCCGGSFSSLSVLIIDHNSVSHSAPFQSCQCMRSIKADNPFQCCCEARE 539
      473 IAFNFLTLPCCSHSRISLVNINENFLLSPSLDFVOSCQEVKTLNAGRNPFRCCELN 532
QY      540 FVKNIQVSSVLEBGPDSYKCDYDESYRGSPLKDFHMEISELSCNITLLIVTIGATMLVLA 599
      533 FIQ-LETSYEVMMQMSDYTCERFANIRGRRLDVLHLSCTTALLIVITIVIMVLG 591
Db      592 LAVAFCCILFDLPWYLRMLGQCTQVHVRKTOBQLRRNRFRHAFISYSHDSIMVXNE 651
QY      600 VTVLSLCIYLDLPWYLRMVCWMTQTRRRARNIPLBELORNIQFPAFTISYSHDSAWKSE 659
      660 LVPYIEKED--IQCLHERNVPGKSIYENIINCIEKSYKSIPIVLSPPFVQSEWCHYEY 717
      652 LIPNLEKEDGSILLCLYESYFDPGKSIENIVSFIEKSYKSIPIVLSPPFVQSEWCHYEY 711
QY      718 FAHNLPFHGSSNNLILILEPIPONSIPNKYHKLKALMTORTYLOMPKESKSGLFMANI 777
      712 FAHNLPFHNSDHTILILIEPIPPCITPTRYHKLKALLEKAYLEMPKDRKCGLFMANL 771
QY      778 RAAFNMKLLVTENNVDKS 796
      772 RAAINVNIAATREMYELQT 790
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RESULT 11
US-09-997-514-57
; Sequence 57, Application US/09997514
; Patent No. 7019116
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Geider, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zenith
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC46
; CURRENT APPLICATION NUMBER: US/09/997,514
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 45.9%; Score 1905.5; DB 3; Length 811;
Best Local Similarity 47.8%; Pred. No. 8, 2e-174;
Matches 382; Conservative 145; Mismatches 251; Indels 21; Gaps 10;

QY 8 IYKSFHVCLMIIY-GRIQSDGNEPAVDKSKRGLIHVPKDLPLKTVLDMSONYIAE 66
DB 3 LIRNIYIFCSIVMTAEGDAPELPEREELMTNCSNMSLRKVPADLTTPATTTDLSTYNLLFQ 62
QY 67 LOVSMSFLSELTVALRSLNRIQLDLSEKFNQOLEYLDLSHNOLOKISCHPIVSFPHL 126
DB 63 LOSSDFHSVSKLRVILCHNRIQLDLKTFEENKELRIDLSSNNRKSVTWYLLAGRL 122
QY 127 DLSFNDPKALPICKEFGNLSQNLFLGASMRLOKDLPLIAHLHSYILLDRNYIKEN 186
DB 123 DLSFNDPDTMPCBAGNMSHLEILGSAKIOKSDFOKIALHILHTVFLGFR--LPHY 180
QY 187 ETESIOILNAKTLHLVFHPTSLFAIQVNI SVNTLGLCLQLTNKLNDNCQVFIKLSLELT 246
DB 181 EEGSIPINTYKGLHIVLPMDTFWILRBDGIKTSKILEWTNI---DGKSGVSY--EMQ 234
QY 247 RGSITLN-----FTLNHIEFTWKCLVRVQPLMPRVEXLVNLT--ISIRREDFY 299
DB 235 RNLSENKTSVLLNKVDLMDPLFLIQFWHTSVBHFQIRNTPFGSKAYLDHNSDFY 294
QY 300 SKTTLKALTIETHTNQVFLSOTALYTVFSENNIMMLTISDPTFIMLCFHPASTFEKLN 359
DB 295 SNTVWRTIKLEHVHRVFIYIQODKLYLLTKMDINLTISNMQHMLFPNPTFOYLN 354
QY 360 FTQNVFTDSIFEKSTLVKLETLIIQKNGKDLFKVGLMTKMPSELEIIVDSWNSLESQR 419
DB 355 FANNILTDELFKRTIQLPHLKTLLNGNKLFTLSVSCFANNTP--LEHIDLSQNLQH-K 412
QY 420 HKNENTWESIYVLLSSNMLTDSVFRCLPRRIKYLUDHSNKIKSVKQVVLKALQELN 479
DB 413 NDENCSWETVVMNMLSTNKLSDSVFRCLPKSIQIILIDNNNOIQVPEKTIHLMALREIN 472
QY 480 VAFNSLTDLPGCGSSLSVLIIIDHNSVHPBADFFQSCOKMRSIKAGDNPQCTCEARE 539
DB 473 IAFNLTDLPGCSHRSLSVLIENNFILSPDLFVQSQEVKTLNAGNPRRCCELKN 532
QY 540 FVKNIQVSEVLEGPDSYKCDYPSYRGSPKDFHNSLSCNTLLITVTIGATMLVIA 599
DB 533 FIQ-LETSEVVMVMSDYTCYCEPLNLRGTRKDVHLELSCNTALLITVIVIMLVLG 591
QY 600 VTVISLCIYLDLPWLRVCCWOTQTRRRARNIPLEIQLNLOPHAFISSEHDSAMVSE 659
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QY 718 FAHNHLFHEGSNNLILILEPIPNISIPNKYHKLKALMTQRTYLOMPKEKSKRGLFWANI 777
DB 712 FAHNHLFHENSDBHILITILEPIPCYCFPRYHKLKALLEKAYULEMPKORRCKGLFWANL 771
QY 778 RAAPFMKTLTVTENNDVKS 796
DB 772 RAATVNVYLATREMYELO 790

RESULT 12
US-09-989-728-57
Sequence 57, Application US/09989728
Patent No. 7029873
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bostein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Dan, L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC72
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Db 235 RNLSENAKTSVLINKVDLMDLDLFLILQFVHTSVSEHFOIRNVTFGKAVLDHNSFDY 294
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Db 295 SNTWRTIKLEHVHVFYIQQDKYVLLTKXDIENLITISNQMDHMLFPNPTFYQYLN 354
Qy 360 FTOVFTDSIFEKSCSTLVKLETLILQKNGLKDLFKVGLMTKMPSELILDVSWNSLESGR 419
Db 355 FANNITDELPRKTTQLPHLKTLLNGKLETLISVSCANNTP--LEHLDLSQNLQK-X 412
Qy 420 HKENCTWVESIVLVNLSNMLTDSVFRCLPPRIKVLDSHKIKSKVQVFKLEALQELN 479
Db 413 NDENCSWPEYVNMNLSYKLSDSVFRCLPKSIQILDINNNOIQTVPKETIHLMALREIN 472
Qy 480 VAFNLTLPFGCGSSSSSVLIIDHNSVSHPSADPFQSQKMSIKAGDNPQCTCELR 539
Db 473 IAFNLTLPFGCGSHRSRLSVLNIEMNFILSPDLFVQSQEVTNAGENPRCTCELN 532
Qy 540 FVKNDQVSEVLEGMPSYKCDYPSYSGSLPKDFHMSLSGNTLLIVTGATMLVLA 599
Db 533 FIQ-LETSSEVMWMSDSYTECEPLNLRGTLLKOVHLSLSCNALLIVTIVMLVIG 591
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Qy 778 RAAFNMKLTLYTENNDVKS 796
Db 772 RAAIVNVLATREMYELQF 790

RESULT 13
US-09-997-349-57
; Sequence 57, Application US/09997349
; Patent No. 7034106
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Geider, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guirney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C37
; CURRENT APPLICATION NUMBER: US/09/997,349
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Db 772 RAAPNKLTVLENNDVKS 790

RESULT 14
US-09-997-653-57
Sequence 57, Application US/09997653
Patent No. 7034122
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
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APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07

PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
Query Match 45.9%; Score 1905.5; DB 3; Length 811;
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67 IQVSDMSELSLTVLRSLSHNRIOQLDLSVFXENODLEYLDSHNOLOKISCHPIVSFRH 126
63 LQSSDFHSVSKRLRYILCHNRIOQLDKTFEENKEIRYLDLSNNRKSXTVYLAGRYL 122
127 DLSFNDPFRALPICXKFGNLSQANFGLSAMKIOKUDLPILALHLSYLLDRNYIKEN 186
123 DLSFNDPFTMPICEBAGNMSHLEIGLSGAKIOKDBFOKIALHLNTPVLFGRY 180
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247 RGSSTLN----FTLNHETWKCLVRVFOFLMPKRVEXLYNIYNTLI--IESIREDEFTY 299
235 RNLSENAKTSVLLNKVDLMDLFLIQFVHTSVSEHFQIRVNTVFGKAYLDHNSFDY 294
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360 FTQNVFTDSIFPEKSTLVYLETILLOKNGLKDLFKVGLMTKMPSELEIDVSNLSR 419
355 FANNITDLERFKRTIQPLKTLILNGKLETLSVSCNANTP--LEHIDLSQNLLOH-K 412
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540 FYKNIDQVSEVLBEAMPDSYKCDYPSYRGSGLKDFHMSLSCNTLILVTIGATMLVLA 599
533 FTQ-LETYSEVMVWQSDSYCEYPLNKGITLKOVHLELSCNRLALVITVIMVLVG 591
600 VTVTSICLYLDLPMYLRWQMTOTRRRANIPLELOQLNLFHAFISYSEHSDAVKSE 659
592 LAVAFCCALFDLPWILRMGQCTQTMHRVRKTTQOLKKNVAFHAFISYSEHSDLVKNE 651
660 LVPYLEKED--IQICHERNVPYKGSIVENIINCIEKSKYSIFVLSPNFVQSEWCHYEY 717
652 LIPNLEKEDGSILICYESYFDPGKISSENIVSFEKSKYSIFVLSPNFVQSEWCHYERY 711
718 FAHNHLFHEGSMNLLIILEPIRONSIPKHYKALKALMQRYLQMPKSKRGCFWARI 777
712 FAHNHLFHENSDDHILILEPIFYCIPRYHKLKALEKAYLEWPKDRKRCGLFWANL 771
778 RAAFNMKLTLVTEENDVKS 796
772 RAAINVNVLATREMYELQ 790
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RESULT 15
US-09-989-293A-57
Sequence 57, Application US/09989293A
Patent No. 7034136
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Denoyers, Luc

APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerltsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
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 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
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 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PIC66
 CURRENT FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 45.9%; Score 1905.5; DB 3; Length 811;

Best Local Similarity 47.8%; Pred. No. 8.2e-174; Matches 382; Conservative 145; Mismatches 251; Indels 21; Gaps 10;

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Qy 8 IVKSFHVCMLTIIV-GTRIQPSDGNFPAVDKSKRGLIHVPKDLPLKTKVLDMSQNYIAE 66
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Db 3 LIRNIYIFCSIVMTAGAPAPLPEBERELMTNCSNMSLRKVPADLPATTTLDLSYNLQ 62
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Qy 67 LOVSMSPLESLTVRLSHNRIOQLDLSVFKNODLEYLDLSHNOLOKTSCHPIVSFRHL 126
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Db 63 LQSSDFHSVSKLRVILCHNRIOQLDKTFEENKEIRYLDLSNNRKSXTWYILAGRLYL 122
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Qy 127 DLSFNDPKALPICKEFGNLSQNLPLGLSAMKLOKLDLPIAHMLSYILDLRNYIYIKEN 186
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Qy 187 ETESQILINAKTLHLVFHPTSLFAIQVNISVNTLGLQLTNLIKLNDDNCQVFIKFLSEL 246
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Qy 247 RGSLLN-----FTLNHIEFTWKCLVRVQFLMPKPEVEVLINLYNLT--IESIREEDFTY 299
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Db 355 FANNILTEBELFRKTIQLPRLKTLINGNLETLISLVSCEPANNTP-LEHIDLSONLLOH-K 412
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 420 HENCSWVESIVVLNLSNMLTDSVFRCLPRLIKVLDLHNNKISKVPKQVVKLEALOELN 479
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Job time : 57 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2006, 23:24:22 ; Search time 527 Seconds
(without alignments)
9774.502 Million cell updates/sec

Title: US-10-732-796A-11
Perfect score: 2753
Sequence: 1 agaatctgacatcatca.....ttcccaatgatctctg 2753

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1 COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
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- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PC/US COMB.seq:*
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- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2749.8	99.9	2758	3	US-09-949-002-226 Sequence 226, App
2	2749.8	99.9	6758	3	US-09-949-002-672 Sequence 672, App
3	2749.8	99.9	6758	3	US-09-949-002-798 Sequence 798, App
4	2748.8	99.8	2760	3	US-09-949-002-100 Sequence 100, App
5	1444.2	51.5	2366	3	US-09-949-002-65 Sequence 65, App1
6	1426.4	51.8	2367	3	US-09-949-002-236 Sequence 236, App
7	1392	50.6	6392	3	US-09-949-002-637 Sequence 637, App
8	1392	50.6	6392	3	US-09-949-002-808 Sequence 808, App
9	777.2	28.2	3462	3	US-09-991-181-56 Sequence 56, App1
10	777.2	28.2	3462	3	US-09-990-444-56 Sequence 56, App1
11	777.2	28.2	3462	3	US-09-997-333-56 Sequence 56, App1
12	777.2	28.2	3462	3	US-09-992-598-56 Sequence 56, App1
13	777.2	28.2	3462	4	US-09-989-735-56 Sequence 56, App1
14	777.2	28.2	3462	5	US-09-989-726-56 Sequence 56, App1
15	777.2	28.2	3462	5	US-09-997-514-56 Sequence 56, App1
16	777.2	28.2	3462	5	US-09-989-728-56 Sequence 56, App1
17	777.2	28.2	3462	5	US-09-997-349-56 Sequence 56, App1
18	777.2	28.2	3462	5	US-09-997-653-56 Sequence 56, App1
19	777.2	28.2	3462	5	US-09-989-293A-56 Sequence 56, App1
20	600.6	21.8	601	3	US-09-949-002-3378 Sequence 3378, App
21	600.6	21.8	601	3	US-09-949-002-8628 Sequence 8628, App
22	540	19.6	601	3	US-09-949-002-2394 Sequence 2394, App
23	540	19.6	601	3	US-09-949-002-9241 Sequence 9241, App

24	337.2	12.2	366	3	US-09-513-999C-25751 Sequence 25751, A
25	189	6.9	21196	2	US-09-949-016-14670 Sequence 14670, A
26	187.4	6.8	2352	2	US-08-889-909A-21 Sequence 21, App1
27	187.4	6.8	2352	2	US-09-156-163A-21 Sequence 21, App1
28	187.4	6.8	2352	3	US-09-982-308B-21 Sequence 21, App1
29	185.2	6.7	601	3	US-09-949-002-2393 Sequence 2393, App
30	185.2	6.7	601	3	US-09-949-002-9240 Sequence 9240, App
31	153.8	5.6	2351	3	US-09-949-016-2928 Sequence 2928, App
32	65.2	2.4	3347	3	US-09-954-987B-169 Sequence 169, App
33	65.2	2.4	3373	3	US-09-954-987B-168 Sequence 168, App
34	63.6	2.3	3150	3	US-09-954-987B-174 Sequence 174, App
35	63.6	2.3	3243	3	US-09-954-987B-173 Sequence 173, App
36	63.6	2.3	3283	3	US-09-999-833A-495 Sequence 495, App
37	63.6	2.3	3283	3	US-10-020-445A-495 Sequence 495, App
38	63.6	2.3	3283	4	US-09-978-189-495 Sequence 495, App
39	63.6	2.3	3283	4	US-10-017-085A-495 Sequence 495, App
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41	63.6	2.3	3283	5	US-10-013-929A-495 Sequence 495, App
42	63.6	2.3	3283	5	US-10-013-917A-495 Sequence 495, App
43	61.2	2.2	3096	3	US-09-954-987B-191 Sequence 191, App
44	61.2	2.2	3220	3	US-09-954-987B-190 Sequence 190, App
45	56.6	2.1	1141	3	US-09-806-708B-22 Sequence 22, App1

ALIGNMENTS

RESULT 1
US-09-949-002-226
; Sequence 226, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CLO00790
; CURRENT APPLICATION NUMBER: US/09/949, 002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 226
; LENGTH: 2758
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-226

Query Match	99.9%	Score 2749.8	DB 3	Length 2758
Best Local Similarity	99.9%	Pred. No. 0		
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			Gaps 0	
QY	1	AGAAATTTGACATCATATCAAGATGCTTGAAGAAGAACACCCCTTAGATGACCATGC	60	
DB	2	AGAAATTTGACATCATATCAAGATGCTTGAAGAAGAACACCCCTTAGATGACCATGC	61	
QY	61	AAACATCATGACCAAGACCAAGACCTATGTTAAAGCTTCATTTTGTTCCTTATG	120	
DB	62	AAACATCATGACCAAGACCAAGACCTATGTTAAAGCTTCATTTTGTTCCTTATG	121	
QY	121	ATCATTAATAGTTGGAACGAGATCCAGTTCGCGGGAATGATTTGACATAGACAG	180	
DB	122	ATCATTAATAGTTGGAACGAGATCCAGTTCGCGGGAATGATTTGACATAGACAG	181	
QY	181	TCAAAAAGAGGCTTATTCATGTTCCAAAGACCTACCGCTGAAAAACCAAGCTTAAAT	240	
DB	182	TCAAAAAGAGGCTTATTCATGTTCCAAAGACCTACCGCTGAAAAACCAAGCTTAAAT	241	
QY	241	ATGTTCTGAACTAATATGCTGAGCTTGAAGCTTCTGACATGAGCTTCTATCAGAGTTG	300	
DB	242	ATGTTCTGAACTAATATGCTGAGCTTGAAGCTTCTGACATGAGCTTCTATCAGAGTTG	301	

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Db 362 AACCGAGATTGAGATTTGATTTGATTTATCTCATTAATCACTTGCAGAAAGATATCCGCCAT 421
QY 421 CCTATTGTGAGTTTCAGGCAATTAGATCTCTCATTCATGATTTTCAGAGCCCTGCCCATC 480
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Db 422 CCTATTGTGAGTTTCAGGCAATTAGATCTCTCATTCATGATTTTCAGAGCCCTGCCCATC 481
QY 481 TGTAAAGAAATTTGGCACTTATCAACACTGAAATTTCTTGGGATGAGTCTATGAAAGCTG 540
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QY 721 ACTTTAGGGTGCTTTCACACTGACTAATTTAAATTTGAATGACAACTGCTCAAGTTTC 780
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QY 781 ATTTAATTTTATTCAGAACTCACAGAGGTTCAACCTTACTGAATTTTACCTCAACACAC 840
| | | | |
Db 782 ATTTAATTTTATTCAGAACTCACAGAGGTTCAACCTTACTGAATTTTACCTCAACACAC 841
QY 841 ATGAAAGAGACTTGGAAATGCTGCTGCTCAAGTCTTTCAAATTTCTTGGCCAAACCTGTG 900
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QY 901 GAATATTCATATTTTACAAATTTTAACTTAATTTGAAGAGATTCGGAAGAGATTTTACT 960
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QY 1081 TCAGATTCACCTTTTATACACATGCTGCTGCTCATGACCAAGCAATTCOAAGTTTTCG 1140
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QY 1141 AACTTTACCCGAAACGTTTTCACAGATAGTATTTTGAAGAAATGTTCCACGTTAGTTAA 1200
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QY 1321 AGACATTAAGAAAGAACTGACTTGGGTTGAGAGTATAGTGTGTTAAATTTGCTTCAAT 1380
| | | | |
Db 1322 AGACATTAAGAAAGAAAGCTGACTTGGGTTGAGAGTATAGTGTGTTAAATTTGCTTCAAT 1381
QY 1381 ATGCTTACTGACTCTGTGTTTCAGAGATTTTAACTTCCAGAGATCAAGGTACTTGATCTTCAAC 1440

Db 1382 ATGCTTACTGACTCTGTGTTTTCAGAGATTTTAACTTCCAGAGATCAAGGTACTGATCTTCAAC 1441
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QY 1501 AATGTGCTTTCATATCTTTTAACTGACCTTCTGAGTGTGCAAGCTTTTACGACCTTTCT 1560
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QY 1621 CAGAGATGAGGTCATTAAGAAAGCAGGGGACAAATCATTCATGATGATCTGAGCTAAGA 1680
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QY 1681 GAATTTGTCAAAAAATATAGACCAAGTATCAAGTGAAGTGTAGAGGGCTGCTGATTTCT 1740
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QY 1801 GAATATTCCTGCAACATTAATCTGCTGATTCGTCACATTCGCTGACCAATGCTGCTGTTG 1860
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QY 1861 GCTGTGACTGTGACCTCTCTCTGTCATCTTGGATTCCTGCTGATTCACAGATGCTG 1920
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Qy 2581 AACAATGTTTTCATCTGGGAACTGAGTACGCGGTGAGGTTAGCCTGCAGTTAGAGAC 2640
Db 2582 AACAATGTTTTCATCTGGGAACTGAGTACGCGGTGAGGTTAGCCTGCAGTTAGAGAC 2641
Qy 2641 AGCCAGTCTCTTCTGGTTTAATCATTAATGTTTCAAAATGAAACAGTCTTTTGAGTAA 2700
Db 2642 AGCCAGTCTCTTCTGGTTTAATCATTAATGTTTCAAAATGAAACAGTCTTTTGAGTAA 2701
Qy 2701 ATGCTAGTTTTCAGTCTCTCCAGTCTGCTTCCCAATGATGATCTGTTG 2753
Db 2702 ATGCTAGTTTTCAGTCTCTCCAGTCTGCTTCCCAATGATGATCTGTTG 2754

RESULT 2

US-09-949-002-672
; Sequence 672, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 672
; LENGTH: 6758
; TYPE: DNA
; ORGANISM: Human
; US-09-949-002-672

Query Match 99.9%; Score 2749.8; DB 3; Length 6758;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 61 AACATCATGACCAAGACAAAGAACCTATGTTTAAAGCTTCCATTTTGTTCCTTATG 120
Db 2062 AACATCATGACCAAGACAAAGAACCTATGTTTAAAGCTTCCATTTTGTTCCTTATG 2121
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Db 2122 ATCATATATGTTGGAACCAAGATCCAGTCTCTCGACGGAATGAATTTGACATAGACAAG 2181
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Db 2242 ATGCTCAGAACTAATGCTGAGCTTCAAGTCTCTGACATAGAGCTTTCTATCAAGTTG 2301
Qy 301 ACAGTTTGAAGCTTCCCATTAACAGAAATCCAGCTACTGATTGAAGTGTTCAGATTTC 360
Db 2302 ACAGTTTGAAGCTTCCCATTAACAGAAATCCAGCTACTGATTGAAGTGTTCAGATTTC 2361
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Db 2362 AACCGAGATTTGAATATTTGGATTTATCTCAATACGTTGCAAAAAGATATCTGCCAT 2421

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Db 2482 TGTAAAGAAATTTGGCAACTTATCAACAGTAAATTTCTTGGATGATGCTATGAAAGCTG 2541
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RESULT 3
US-09-949-002-798
; Sequence 798, Application US/09949002
; Patent No. 690016
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 798
; LENGTH: 6758
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-798

Query Match 99.9%; Score 2749.8; DB 3; Length 6758;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 2; Indels 0; Gaps 0;
Matches 2751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 61 AACATCATGACCAAGAAAGAAAGAACTATTTGTTAAAGCTTCCATTTTGGCTTATG 120
Db 2062 AACATCATGACCAAGAAAGAAAGAACTATTTGTTAAAGCTTCCATTTTGGCTTATG 2121
Qy 121 ATCATTAATAGTTGAACAGAAATCCAGTTCCTCCGACGGAATGAATTGACATAGACA 180
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RESULT 5

US-09-949-002-65
; Sequence 65, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: C1000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 2366
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-65

Query Match 52.5%; Score 1444.2; DB 3; Length 2366;
Best Local Similarity 76.4%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 548; Indels 6; Gaps 1;

88 ATTTGTTAAAGCTTCATTTTGTGCTTATGATCATATAGTGGAGAACCAATCCAG 147
1 ATGACATGACATTTCCATTTTCCATTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTAT 60
148 TTCTCCGACGGAATATGATTTGACATGACAGTCAAAAGAGCTTTATGATGCTCA 207
61 TATCTGAAGAAAGGAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
208 AAAGACTTACCGCTGAAAACCAAGCTTTAGATGATGCTCAGAACTACATGCTGAGCTT 267
121 AAAGACTTACCGCTGAAAACCAAGCTTTAGATGATGATGATGATGATGATGATGATGATGATGATG 180
268 CAGGCTCTGACATGAGCTTTCTATCAGAGTGAAGATTTGAGCTTTCCATTAACAA 327
181 TGGACTTCTGACATCTTATCTGCTGCAAAAGAGATTTGATGATGATGATGATGATGATGATGATGAT 240
328 ATCCAGTACTGATTTAAGTGTTCAGAGTCAACAGAGATTTGATGATGATGATGATGATGATGATGAT 387
241 ATCCAGTACTGATTTAAGTGTTCAGAGTCAACAGAGATTTGATGATGATGATGATGATGATGATGAT 300
301 TCCCAACAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
388 TCTCATTAATCACTTGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 447
448 CTTCTATCAATGATTTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 507
361 CTGTATTTAATGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
508 CTGAATTTCTTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567
421 CTGAATTTCTTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
568 CACTTGCATCTAAGTATATCTTGTGATTTAGAAATTTATATATATATATATATATATATATATATAT 627
481 CATTGAATATCAGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
628 ACAGAAAGCTTACCAATTTCTGAATGCAAAACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 687
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688 TTATTCGCTATCCAGTGAACATATCACTTATATCTTATAGGATGCTTCAACTGACTAAT 747
601 GAATTCATTTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
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QY	802	ACCGAGGTTCAACCTTACTGAATTTTACCTCCACCAACATRAGAAACGACTTGGAAATGC	861
Db	721	CAAAACAAATCCAAAGTTATCAAGTCTTAACTTTAAACCAATGGAAACAACTGGAAATCTT	780
QY	862	CTGGTCAGAGTCTTTCAAATTTCTTTGGGCCAAACCTGGGAATATCTCAATATTTCACAT	921
Db	781	TTCAATTAGGATCTCCAGCTGTTTGGCATACACTGATATGTATTTCTCAATTTTCAAC	840
QY	922	TTAACAATAATTGAAAGCATTCGGAGAAAGATTTTACTTATTTCTAAACGACATTGAA	981
Db	841	GTGAAGCTACAGGGCTCAGCTGGACTTTCAGAGATTTTGTATTTCTGGCACTCTCTTGAAG	900
QY	982	GCATTGACAATATGAACATATACGAAACCAAGTTTTTCTGTTTTCACAGACGCTTGTAC	1041
Db	901	GCTTGTCTAATACCAAGAGTGTCCGCAATGTTGCGGTTTTTCGCAAAAGTTATATCTAT	960
QY	1042	ACCGGTTTTCTGAGATGAACATTTATGATGTTTAACATTTCAGATACACCTTTATACAC	1101
Db	961	GAAATCTTTTGCAATATATGACATTCAAAAATTTCAAGTGTCTGGTACACGATGGTCCAC	1020
QY	1102	ATGCTGTGTCTCATGACACCAAGACATTCAGTTTTTGAACCTTTACCAGAACGTTTTTC	1161
Db	1021	ATGCTTTGCCCATCCAAATATTAAGCCCGTTCCGACATTTGGATTTTTTCCAAATATCTGTA	1080
QY	1162	ACAGATAGTATTTTGAAGAAATGTTTCCACGTTAGTTAATTGGAGACCTTATCTTACAA	1221
Db	1081	ACAGACACGGTTTTTGAAGAAATTTGTGGGACCTTACTGATTTGGAGACCTTATTTTTCAA	1140
QY	1222	AAAAATGATTTAAAGACCTTTTCAAAGATGGTCTCAGACGAGAGGATATGCTCTTGTG	1281
Db	1141	ATGATATCAATTTAAAGAACTTTCAAAAATAGCTGAAGAAAGACTACACAGATTAAGTCTCTG	1200
QY	1282	GAAATACTGATGATGTAGCTGTGGAATCTTTGGAATCTGTGTAGACATTAAGAAACGTGCACT	1341
Db	1201	CAACGATTTGGATATATAGCCAGAAATCTGTAAAGCTATGATGAAGAAAGAGACGTGTTCT	1260
QY	1342	TGGGTTGAGATATAGTGGTGTAAATTTGTCTTCAAAATATGCTTACTGACTCTGTTTTC	1401
Db	1261	TGGACTTAAAGTTTATTTAAATTTAAATTTATGTTCTTCAAAATTAATCTTACGACATATTTTTC	1320
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QY	1522	ACTGACCTTCTCGATGTGGACGCTTTTAGACAGCTTTCTGTATGTATCATTTGATCACAT	1581
Db	1441	ACTGACCTTCTCGATGTGGACGCTTTTAGACAGCTTTCTGTATGTATCATTTGATCACAT	1500
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Db	1801	TGCATCTACTTGGAATCTGCGCTGGTATCTAGAGATGGGTGTGCCAGTGGACCCGACC	1860
QY	1942	CGCAGGGCCAGGAACATACCCCTTAGAAGAATCCCAAGAAACCTCCAGTTTCATGCTTTT	2001
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Db	1921	ATTTCATTAATGAGAACATGATTCCTGGGTGTAAAAGTAATTGGTAATCCTTACCTAGAA	1980
QY	2062	AAGAAGATPATACAGATTTTGTCTCATGAGAGAACTTTGTCCCTGGCAAGACATTGTG	2121
Db	1961	AAAGAGGTATGCAGATTTTGTCTCATGAGAGAACTTTGTCTGGCAAGAGATTGTG	2040
QY	2122	GAAAAATATCATCACTGCATTGAGAGAAGTTACAGATTCATCTTTGTGTCTCCAC	2181
Db	2041	GAAAAATATCATCACCTGCATTGAGAGAAGTTACAGATTCATCTTTGTGTCTCCAC	2100
QY	2182	TTTTGTCCAGAGTGTGTGTGCTTACAGAACTATTTTGGCCATGCAATCTCTTTTCAT	2241
Db	2101	TTTTGTCCAGAGTGTGTGTGCTTACAGAACTATTTTGGCCATGCAATCTCTTTTCAT	2160
QY	2242	GAGGATCTATACTTAATCTTATCTCATCTTPACTGGAACTTCACAGAACAGATCTCC	2301
Db	2161	GAGGATCTATACTTAATCTTATCTCATCTTGTGCTGAACTTCACAGAACAGATCTCT	2220
QY	2302	AACAAGTACCAAGCTGAAAGCTCTCATGACGACGCGACTTAATTTGCAGTGGCCCCAG	2361
Db	2221	AGCAGTTATATCAACAGCTCAAAAGCTCATGCGCCAGAGGACCTTAATTTGGAATGGCCCCAG	2280
QY	2362	GAGAAAGCAAAGCTGGGCTCTTTTGGGCTPAACATTTAGACCGCTTTTAATATGAATTA	2421
Db	2281	GAAAAAGCAAACCTGGGCTCTTTTGGGCTPAACATTTAGAGGACGACCTTAATTTAAGCTG	2340
QY	2422	ACA 2424	
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RESULT 6			
US-09-949-002-236			
; Sequence 236, Application US/09949002			
; Patent No. 6900016			
; GENERAL INFORMATION:			
; APPLICANT: VENTER, J. Craig et al.			
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED			
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION			
; FILE REFERENCE: CLO00790			
; CURRENT APPLICATION NUMBER: US/09/949,002			
; CURRENT FILING DATE: 2000-01-28			
; PRIOR APPLICATION NUMBER: 60/231,401			
; PRIOR FILING DATE: 2000-09-08			
; NUMBER OF SEQ ID NOS: 10823			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 236			
; LENGTH: 2367			
; TYPE: DNA			
; ORGANISM: Human			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (1)..(2367)			
; OTHER INFORMATION: n = A,T,C or G			
US-09-949-002-236			
Query Match 51.8%; Score 1426.4; DB 3; Length 2367;			
Best Local Similarity 76.1%; Pred. No. 0;			
Matches 1785; Conservative 0; Mismatches 552; Indels 8; Gaps 2;			
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1801 TCTGATCTACTTGGATCTGCTGCTGATCTGATGCTGCTGCTGCTGCTGCTGCTGCT 1860
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2240 ATGAAGATCTAATTAATCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 2299
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QY 1615 AGCTGCAGAGATGAGTCAATTAAGAGAGGAGCAATCCATTCATGTACTGTAG 1674
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QY 1675 CTAAAGAAATTTGTCAAAATATAGCAAGTATCAAGTGAAGTGTAAAGGCTGGCT 1734
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DB 3621 CTAAAGAAATTTGTCAAAATATAGCAAGTATCAAGTGAAGTGTAAAGGCTGGCT 3680
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QY 1735 GATTCCTTAAGTGTACTGACCAAGATTAAGAGAGGAGCAATTAAGGACTTTCAC 1794
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DB 3681 GATTCCTTAAGTGTACTGACCAAGATTAAGAGAGGAGCAATTAAGGACTTTCAC 3740
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QY 1795 ATGTCTGAATTAATCTGCAACATTAATCTGTGATGTACCAATCCGATGCTG 1854
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DB 3741 ATGTCTGAATTAATCTGCAACATTAATCTGTGATGTACCAATCCGATGCTG 3800
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QY 1855 GTGTGGCTGTGACTGTGACCTCTCTGATCTACTGTGATCTGCTGTGATCTCAG 1914
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QY 2335 CAGCGGACTTATTTGAGTGGCCCAAGAGAAAGCAAGCTGGGCTTTTGGGCTTAC 2394
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RESULT 8
US-09-949-002-808

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; Sequence 808, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 808
; LENGTH: 6392
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6392)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-808

Query Match      50.6%; Score 1392; DB 3; Length 6392;
Best Local Similarity 75.3%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 552; Indels 33; Gaps 3;

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QY 601 AGAAATTAATTAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTA 660
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DB 2541 AGAAATTAATTAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTA 2600
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| | | | |
DB 2721 GTTTTCATTAATTTTATCAAGATCTACAGAGGTTCACTTACCTTACCTTACCTTAC 2780
| | | | |
QY 835 AACCATTAAGAAACGATTTGGAATGCTGTGACAGTCTTTCAATTTCTTTGGCCCAA 894
| | | | |
DB 2781 AACCATTAAGAAACGATTTGGAATGCTGTGACAGTCTTTCAATTTCTTTGGCCCAA 2840
| | | | |
QY 895 CCTGTGAATATCTCAATATTTCAATTTAACAATTAATTTGAAGCATTCGTGAAGAGAT 954
| | | | |
DB 2841 CCTGTGAATATCTCAATATTTCAATTTAACAATTAATTTGAAGCATTCGTGAAGAGAT 2900
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;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 28.2%; Score 777.2; DB 3; Length 3462;
Best Local Similarity 59.8%; Pred. No. 3e-209;
Matches 1456; Conservative 0; Mismatches 948; Indels 30; Gaps 8;

QY 45 TTAGATAGCCACTGCACATCATGACCAAGACAAAGACCTATTGTTAAAGCTTCCA 104
DB 77 TGAGGAATTAAGTGGTAAATCCTTGGAAATACAAATGACACTCATCAGAAACATTTACAT 136
QY 105 TTTTGTGGCTTATGATATATAAGTTGGAACAGAAATCCAGTTCTCCGAGGAAATGA 164
DB 137 ATTGTGATATTGTTATGACAGAGGGTGATGCTCCAGAGCTGCCAGAAAGGGA 196
QY 165 ATTGCAGTAGACAAAGTCAAAAAGAGGCTTATTCATGTTCCAAAAGACCTACCGCTGAA 224
DB 197 ACTGATGACCAACTGCTCCACATGCTCTTAAAGAAAGTTCCCGCAGATTTGACCCAC 256
QY 225 AACCAAGCTTAGATATGCTCAGAACTACATCGCTGAGCTTCAGGCTCTGACATGAG 284
DB 257 CACAAAGCACTGATTTATCTATPAACTCCCTTTTCACTCCAGAGTTCCAGATTTTGA 316
QY 285 CTTTCTATCAGAGTTGACAGTTTGGAGCTTTCCCAATAAGATCCAGTACTGATTT 344
DB 317 TTCTGTCTCCAACTGAGAGTTTGAATCTATGCCATTAACAGAAATCAACAGCTGATCT 376
QY 345 AAGTGTTCAGATTCACAGAGATTTGAATATTTGGATTTATCTCATATACATTTGA 404
DB 377 CAAAACCTTGAATTCACAGAGATTTAGATATTTAGATTTGTCTAATACAGACTGA 436
QY 405 AAAGATATCTGCCATCTATTTGTGAGTTTCAGGCAATTAGATCTCTCATTCATGATTT 464
DB 437 GAGTGAATCTGTATTTACTGGCAGGCTCAGGATTTTGAATCTTTTAAATACAT 496
QY 465 CAAGCCCTGCCATCTGTAAGAAATTTGGCAACTTATCACAACGAAATTTCTGGGAT 524
DB 497 TGACACCAATGCTATCTGTAGAGAGCTGGCAACATGTCAACCTGAAATCTTAGGTT 556
QY 525 GAGTGTATGAGCTCAAAAATTTAGATTTGCTGCCAATTTGCTCACTTCATCTAAGTTA 584
DB 557 GAGTGGGCAAAAATTCAAAATTCAGATTTCCGAAAATTTGCTCATCTGCATCTAAATAC 616
QY 585 TATCTCTTGAATTTAAGAAATTTATTAATAAAGAAATGAGACAGAAAGTCTACAAT 644
DB 617 TGTCTTCTTAGAGTTTCAAGACTCTTCTCT-----CATTAAGAAGAGTAGCTGCCAT 670
QY 645 TCTGAATGCAAAACCTTCACTTGTGTTTTCACCCCACTAGTTTATGGCTATCCAAAT 704
DB 671 CTTAAACAGCAAAAATGACACTGATTTTAAACCAATGACACAATTTCTGGGTTCTTTT 730
QY 705 GAAACATATGATTAATATCTTTAGGGTGTACCAACTGACATAATTAATTAATGAATGA 764
DB 731 GGTGATGGAATCAGACTTCAAAATATTTAGAAATGACAAAATTA-TAGATGCAAAAGCC 789
QY 765 CAAGTGTCAAGTTTCAATTAATTTTATCAGAACTCACAGAGGTTCAACTTACTGAA 824
DB 790 AATTGTGATGTTATGAATGCAAGAAATCTTAGTTAAGAAATGCTAAGAC--ATCGGT 847
QY 825 TTTTACCTCAACCAATGAAAGCACTTGGAAATGCTGGTCTGAGAGTCTTTCAATTTCT 884
DB 848 TCTATTGCTTAATAAAGTGTATTAATCTGGGAGCAACTTTTCTTATCTTACAAATTTGT 907

QY 885 TTGGCCCAACCTGTGGAATATCTCAATATTTAACAATTTAACAATTAATGAAGACTTCG 944
DB 908 TTGGCATCATCAGTGGAAACCTTTCAGATCCGAATGTGCTTTGTGTGAAGGCTTA 967
QY 945 TGAGGAAGA-----TTTATCTTATTCATAAAGCAATTTGAAGCATTTGACATAGAA 998
DB 968 TCTTGACCAATTCATTTGACTACTCAAAATCTGTATGGAATGAACTATAAATTTGAGCA 1027
QY 999 TATCAGAACCAAGTTTTCGTGTTTCAAGACAGCTTTGTACACCGTGTTCGAGAT 1058
DB 1028 TGTACATTTCAAGTGTGTTTCAATTCACAGAGTAAATCTATTGTCTTTGACCAAAAT 1087
QY 1059 GAACATTTATGATTTAACATTTGAGATGACCTTTTATACATGCTGTCTCTCAATGC 1118
DB 1088 GGACATTAAGAAACCTGCACAAATATCAAAAGCAAAATGCAACATGCTTTTCCGAATTA 1147
QY 1119 ACCAAGCACTTCAAGTTTGAACCTTACCAGAGCTTTTCACAGATAGTATTTTGA 1178
DB 1148 TCTTAGAAATTCAAATATTTAAATTTGGCAATATATCTTTACAGACGAGTGTTTAA 1207
QY 1179 AAAATGTTCCAGTGTAGTTAAATTTGAGACACTTATCTTACAAAAAATGGAATTAAGA 1238
DB 1208 AAGACTATCCAACTGCCTCACTTGAAGAACTCATTTGATGGCAATTAATCGAGAC 1267
QY 1239 CTTTTCAAAGTAGTCTCATGACGAGAGATATGCTTTCTTTGAAATATCTGATGTTAG 1298
DB 1268 ACTTCTTATGATTAAGTCTTTGCTTACAAACACAC--CCTTGGAAACCTTGGATCTGAG 1324
QY 1299 CTGGAATCTTTGGAATGTGGTAGACATAAAGAAATGCACTGGGCTGAGAGATAGT 1358
DB 1335 TCAAAATCTATTACAC--ATAAATGATGAATTTGCTCATGCGCAAAACCTGTGT 1381
QY 1359 GGTGTAAATTTGCTTCAAAATATGCTTATGACTCTGTTTTCAGATGTTTACCTCCAG 1418
DB 1382 CAATATGATCTGTATCAATTAATGTCTGATCTGTCTTCAAGTCTTGGCCAAAG 1441
QY 1419 GATCAAGTACTGATCTTCCACAGCAATTAATTAAGAGCTTCTTAACAAGCTGTAA 1478
DB 1442 TATTCAAAATCTTGACTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1501
QY 1479 ACTGAAGCTTTGCAAGAACTCAATGCTTTCATTTCAATCTTTAATGACTCTTCTGATG 1538
DB 1502 TCTGATGGCTTACAGAACTTAATATGCAATTTATTTTCTAATGATCTTCCCTGATG 1561
QY 1539 TGGCACTTTTGAACCTTTCTGATTTGATGATGATGATCAATTTGATTTCCACCATC 1598
DB 1562 CAGTATTTCAATGATCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1621
QY 1599 GGTATATTTCTTCCAGAGCTGCAGAGATGAGTCAATTAAGAGAGGAGCAATTCAT 1658
DB 1622 TCTGATTTTGTTCAGAGCTGCAGAGATTTAAATCTTAATGCGGAGAGAAATCCAT 1681
QY 1655 CCAATGTACTGTGAGCTTAAGAAATTTGTCAAAAATTAAGCAAGTATCAAGTGAAT 1718
DB 1682 CCGGTGACCTGTGAATTA--AAATTTCTTACGCTTGAACATATTTAGAGTCAAT 1738
QY 1719 GTTAGAGGCTGGCTGATTTCTTATAGTGACTATCCAGAAATTTATAGAGAGCC 1778
DB 1739 GATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1798
QY 1779 ACTAAGGACTTTCATGCTGATTAATCTGCAACATTAATCTGCTGATGCTGATCAAT 1838
DB 1839 GGTGACCAATGCTGT 1898
QY 1859 TGTGTATTTATGCTAGTCTGTGGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1918
QY 1899 GGCCTGTATCTCAGAGATGTTGCAAGTGAACCCAGACTCGGCGCAGGAGGCAAGT 1958
DB 1919 GCTCTGTATCTCAGAGATGCTAGTCAATGCAACAAATATGCAAGGTTAGGAAAC 1978
QY 1959 ACCCTTAGAAGAACTCCAAAGAACTCAGTTTCAATGCTTTTATTAATTAATGTAACA 2018

;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
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;; PRIOR APPLICATION NUMBER: 60/090863

;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 28.2%; Score 777.2; DB 3; Length 3462;
Best Local Similarity 59.8%; Pred. No. 3e-209;
Matches 1456; Conservative 0; Mismatches 948; Indels 30; Gaps 8;

QY 45 TTAGATAGCCACTGCATCATATGCAAGACAAAGAACCTATTGTTAAAGCTTCA 104
DB 77 TGAGGAAATAAGTGTAAATCTTGAAATACATGAGACTCATGAAAATTATCAT 136
QY 105 TTTTGTGGCTTATGATCATATATAGTGAACCAATCCAGTCTCCGACGAAATGA 164
DB 137 ATTTGTGTATTTGTTATGACGACGAGGATGATGCTCCAGCTGCCAAGAAAGGA 196
QY 165 ATTTCAGTAGCAAGTCAAAAAGAGCTTATTCATGTTCCAAAAGCTTACGCTGAA 224
DB 197 ACTGATGACCAACTGCTCCACATGCTCTTAAGAAAGGTCCCGAGACTGACCCGAC 256
QY 225 AACCAAGCTTAGATATGATGTCAGAACTACATGCTGAGTCTGACATGAG 284
DB 257 CACCAACGACACTGAGTTATCTATTAACCTCTTTTCACTCCGAGTTCAGATTTCA 316
QY 285 CTTTCTATCAGAGTTGACAGTTTGAAGCTTCCATTAACAGATCCAGCTTATGATTT 344
DB 317 TTTCTCTCAACTGAGAGTTTATTTATGCTCATTAACAGATTTCAAGCTGATCT 376
QY 345 AAGTCTTTCAGTTCACACGAGATTTGAATATTTGATTTATCTCAATCACTTGA 404
DB 377 CAAAACCTTGAATTCACACAGAGTTAAGATTTGATTTGTTAATTAACAGCTGAA 436
QY 405 AAAGATATCTGCTCATTTATGATGATTTGAGGATTTAGATTTGATCTCATTCATGATTT 464
DB 437 GAGTGTAACTGGTATTTACTGGCAGGCTCAGGATTTAGATTCCTTTTAAAGACTT 496
QY 465 CAAGGCCCTGCCCATCTGTAAGGAATTTGGCACTTATCACAGTAATTTCTTGGAGTT 524
DB 497 TGACACCATGCTTATCTGTGAGAACTGGCAACATGTCACACTGGAAATCTTAGGTTT 556
QY 525 GAGTCTATGAGCTGCAAAATTTGATTTGCTGCAATTTGCTCATTTGATCTTAAGTTA 584
DB 557 GAGTGGGGAAATAATCAAAAATTCAGATTTTCCAGAAATTTGCTCATTCGATCTTAATAC 616
QY 585 TATCTCTTGATTTAAGAAATTTATATTAATAAAGAAATGAGACAGAAAGCTTCAAT 644
DB 617 TGTCTTTTAGGATTCAGAACTTCTCTCT-----CATATGAAGAAGGTAGCTTCCAT 670
QY 645 TCTGAATGCAAAACCTTCACTGTTTTCACCAACTGTTATTTGCTATCCAGT 704
DB 671 CTTAAACACAAACCTGACATTTTACCAATGACACAAATTTCTGGGTTCTTTT 730
QY 705 GAACATATCAGTTAATCTTATGAGGTGCTTACCACTGATCTAATATTAATTAATGATGA 764
DB 731 GCGTATGGAATCAAGACTTCAAAAATTTAAGAAATGCAATA-TAGATGCAAAAGCC 789
QY 765 CAACGTCAAGTTTCAITTAATTTTATCAGAACTCACAGAGTTCAACTTACTGAA 824

[illegible]


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, PRIOR APPLICATION NUMBER: 60/090695
, PRIOR FILING DATE: 1998-06-25
, PRIOR APPLICATION NUMBER: 60/090696
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, PRIOR APPLICATION NUMBER: 60/092182
, PRIOR FILING DATE: 1998-07-09

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Query Match	28.2%	Score 777.2;	DB 3;	Length 3462;
Best Local Similarity	59.8%;	Prod. No. 3e-209;		
Matches 1456;	Conservative	0;	Mismatches 948;	Indels 30;
			Gaps	8;
QY	45	TTAGATAGCAGTCGCAACATCATGACCAAAAGACAAAGAACCCTATTTGTTAAAGCTTCA	104	
Db	77	TGAGGAATTAAGTGGTAAATCTCTTGGAAATACAAATGAGCTCATCAGAAACATTTCAT	136	
QY	105	TTTGTGTTCCTTATGATCATTAATAGTTGGAACCGAATCCAGTTCTCCGACGAATGA	164	
Db	137	ATTTTGATGATTTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAGAAAGAAAGGA	196	
QY	165	ATTTCAGTAGACAAAGTCAAAAAGAGCTTATTTCATGTTCCAAAAGCTACCGCTGAA	224	
Db	197	ACTGATGACCAACTGCCTCCAACTGCTCTTAAGAAAGGTTCCCGACGCTTGACCCACGC	256	
QY	225	AACCAAGTCTTAGTATGTCGCAATTAATATGCTGAGCTTCAGGCTCGACATGAG	284	
Db	257	CACACGACACTGGATTATTCCTATACCTCTTTTCAACTCCAGAGTTCAAGATTTTCA	316	
QY	285	CTTTCATACAGATGACAGTTTGTGAGCTTCCCATACAGAAATCCAGTACTTATTT	344	
Db	317	TTCTGTCCCAACTGAGAGTTTGATTCATATGCATTAACGAATTCACAGCTGAGTCT	376	
QY	345	AAGTGTTTCAAGTTCAACCGAGATTTGAAATTTGGATTATCTCAATATCAGTTGCA	404	
Db	377	CAAAACCTTGAAATTCACCAAGGAGTAAAGATTTAATTTGTTCTTAATTAACAGACTGA	436	
QY	405	AAAGATATCCGCGCATCCTATTTGGAGTTTCAGGATTTAGATCTGCATCAATGATTT	464	
Db	437	GAGGTAACTTGGATTATCTGGCAGGCTCCAGGATTTAAGTCTTTCTTTTAATGACTT	496	
QY	465	CAAGGCCCTGCCACTCTGTAAAGAAATTTGGCAACTTATCACAACGAAATTTCTTGGAGTT	524	
Db	497	TGACACCATGCTATCTGTGTAGGAAGCTGGCAACTGTACACCTGGAAATCTTAGGTTT	556	
QY	525	GAGTGCTATGAAAGCTCAAAAATTAGATTGCTGCAATTGCTCATTTGACTTAAGTTA	584	
Db	557	GAGGGGGCAAAAATACAAAATACAGATTTCCAGAAAATTCCTCATCGCACTTAATAATC	616	
QY	585	TATCTCTCTGATTTTAAGAATTTATATATAAAGAAATGAGACAGAAAGCTTCAAT	644	
Db	617	TGTCTTCTTGAAGATTCAAGACTTTCCCT-----CATTTGAGAAGAGTACCTGCCAT	670	
QY	645	TCGATATGCAAAAACCTTCACTTGTGTTTTTCACCCAACTAGTTTATTCGCTATCAAGT	704	

D	b	672	CTTAAACACAAACAACTGCACATGTTTTCACATGAGACAAATTTTCGGTCTTTT	730
Q	y	705	GAACATATGACGTTAATACTTTAGGGGCTTACCACTGACTAATATTAATGAATGATGA	764
D	b	731	GGGTGATGGAAATCAAGACTTCAAAAATATATAGAAATGACAAATA-TAGATGGCAAAAGCC	789
Q	y	765	CAACTGTCAAGTTTCATTAAATTTTTCATCAGAACTCACAGAGTTCAACTTACTGAA	824
D	b	790	AAATTGTAAGTATGAAATGAACAGAAATCTTAGTTTGAAAAATGCTAAGAC--ATCGGT	847
Q	y	825	TTTTTACCCTCAACCAATATGAAACGCTTGGAAATAGCCGGGACAGGCTTCAATTTCT	884
D	b	848	TCTATTGCTTAATAAGTGATTTTACTCTGGAGCACTTTTCTTATCTTCAAAATTTGT	907
Q	y	885	TTGGCCCAAAACCTGTGGAATATCTCAATATTTTACATTTAACTAATATGGAACATTCG	944
D	b	908	TTGGCATACATCAGTGGAACTTTACAGATCCGAATATGACTTTTGGGTAAAGCTTA	967
Q	y	945	TGAAGAAGA-----TTTACTTATTTCTTAAAACGACTTGAAGAGCTTGACATATGACA	998
D	b	968	TCTTGACCAACAATTCATTTGACTACTCAAAATCTGATATGAGAACTAATAAAATGGAGCA	1027
Q	y	999	TATCAGAAACCAAGTTTTCGTGTTTCCAGACAGCTTTGACACCGTGTTCGTGAT	1058
D	b	1028	TGTACATTTCAAGTGTGTTTACATTCACAGGATTAATAATCTATTTGCTTTTGACCAAAAT	1087
Q	y	1059	GAACATTTATGATGTATTAACCATTTCCAGATACACCTTTTATACAGATGCTGTCTCATGC	1118
D	b	1088	GGACATATGAAAACTGACAAATATCAAAATGACAAATGGCACAGATCTTTCCCGAATTA	1147
Q	y	1119	ACCAAGCACATTCAGTTTGTGAACTTTACCAGAGCGTTTCCAGATATATTTTGA	1178
D	b	1148	TCTTAGAAATTCAAATATTTTAAATTTTGGCCAAATATCTTAAACAGACAGATGTTTAA	1207
Q	y	1179	AAATGTGCCAGTTATGTTAAATTTGAGACACTTATCTTACAAAAAATGATTTAAAGA	1238
D	b	1208	AAAGATATATCCAACTGCCCTCACCTTGAACCTCTCATTTTGAATGGCAATAAATCGGAGAC	1267
Q	y	1239	CCTTTTCAAAGTAGGCTCATGACGAGATATGCTCTTTTGGAAATATCGAATGTTAG	1298
D	b	1268	ACTTTCTTAGTAAGTTGCTTTGCTTACACACAC--CCTTGGACACTTTGATCTGAG	1324
Q	y	1299	CTGGAATTCCTTGAATCTGTAGACATTAAGAAAACTGCACCTTGGTTGAGATATAGT	1358
D	b	1325	TCAAAATCTATTAACAAC--ATTAATAATGATGAATAATTTGCTCATGGCCAGAAATGTGGT	1381
Q	y	1359	GGTGTAAATTTGTCTTCAATATATGCTTACCTGTCTTTCAGATGTTTACCTCCAG	1418
D	b	1382	CAATATGAATCTGTCTAATCAATAAATTTGTGATTTCTGTCTTCAGTGCCTTGGCCAAAG	1441
Q	y	1419	GATCAGAGTACTGATCTTCAAGAGAAATTAATAAGAGGCTTCTTAAACAAGTCGTAA	1478
D	b	1442	TATTCAAAATACCTGACCTTAATTAATTAACCAATCCAACTGTACTTAAGGACTATTTCA	1501
Q	y	1479	ACTGGAAGCTTTGCAAGAACTCAATGTTGCTTTCAATCTTTAACTGACCTTCCGTGATG	1538
D	b	1502	TCTGATGGCTTACAGAGAACTAAATATTTGATTTATTTTCTTAATCTGATCTCCCTGATG	1561
Q	y	1539	TGGCAGCTTTAGCAGCCTTTCTGTATGATCATTTGATCACAATTCAGTTTCCACCCATC	1598
D	b	1562	CAGTCAATTCAGTAAGACTTTCAGTTCTGACATTTGAATGAATTCATTTCTCACCCCATC	1621
Q	y	1599	GGCTGATTTCTTCCAGAGCTGCCAAGATGAGTGCATAAACACAGGACCATTCATTT	1658
D	b	1622	TCTGGATTTTGTTCAGAGCTGCCAAGAGTTTAAATCTTAATATCGGGAGAAATTCATTT	1681
Q	y	1659	CCAATATCACTGTGACTTAAGAGAAATTTGTCAAAAATATAGACCAAGATATCAAGTGAAGT	1718
D	b	1682	CCGGTATCACTGTGAATTA---AAAATTCATTCAGCTTGAAACATATTCAGAGGTGAT	1738
Q	y	1719	GTTTAAAGGGCTGCCGCTGATTTCTTATTAAGTGTGACTACCCAGAAAGTTATAGAGAAAGCC	1778
D	b	1739	GATGATTTGATGTGATGATTAATCAACCTGTGAATATCCCTTTAAACCTTAAGGGGAACTAG	1798

1779 ACTAAGAGCTTTCACATGTCGTAATTAATCCGCAACATAACTCTGTCGTCACCAT 1838
1799 GTTAAABAACGCTTCTCTCCAGAAATTAATCTTGCAACACAGCTCTGTCATGTCACCAT 1858
1839 CGGTGCCACCATGCTGCTGTTGGCTGTGACCTGTCGTCATCTTCTGATCT 1898
1859 TGTGATTAATAGCTAGATTTCTGGGCTGTGCTGCTCTGCTCTCCACTTTGATCT 1918
1899 GCCCGGATCTCAGAGATGTCGTCAGTCGACCCAGACTGGGCCAGGCCAGAACAT 1958
1919 GCCCGGATCTCAGAGATGTCGTCAGTCGACCCAGACTGGGCCAGGCCAGAACAT 1978
1959 ACCCTTAGAAGACCTCCAAAGAAACCTCCAGTTTCATGCTTTTATTTATAGTGAACA 2018
1979 AACCCAAAGAACCTCCAAAGAAAGTCCGATTTCCAGCATTTATTTCTAAGAGAAC 2038
2019 TGATTCCTGCTGGTGAAGAAAGTGAATGGTACCTTAAGTGAAGAAAGAAAGAA- -TAT 2072
2039 TGATTCCTGCTGGTGAAGAAAGTGAATGGTACCTTAAGTGAAGAAAGTGAAT 2098
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2099 CTGATTTGCTTTCATGAGAGAACTTGTCCGCAAGACATTTGCGAAATATATGT 2158
2133 CAACCTGATGAGAGAGTTACAGTCCATCTTTGTTTGTCTCCCACTTGTCCAGAG 2192
2159 AAGCTTCAATGAGAAAGTAAAGTCAATCTTTGTTTGTCTCCCACTTGTCCAGAA 2218
2193 TGAGTGGTCCATTAAGAACTTATTTGGCCATCAAACTCTTTCATGAGAGATCTAA 2252
2219 TGAGTGGTCCATTAAGAACTTATCTTGGCCACCAAACTCTTTCATGAGAAATCTGA 2278
2253 TAACCTAATCTCAATCTTAATGGAACCCATTTCCACAGAACAGATTTCCCAAAATGACA 2312
2279 TCAATTAATCTTAATCTTAATGGAACCCATTTTCATTTCCACAGAGATCA 2338
2313 CAAGCTGAAGGCTCATGAGCAGCGGACCTTATTTGCGCCCAAGAGAAAGCA 2372
2339 TAAATGAAAGCTCTCCGCAAGAAAGCAATCTTGGAATGCGCCAGAGATGACGCTAA 2398
2373 ACGTGGGCTCTTTTGGCTTAACATTAAGCCGCTTTTAAATGAATTAACCTAGTAC 2432
2399 ATGTGGGCTTTTCTGGGCAACCTTCAAGCTCTTAATGTAATGTAATGTCACACG 2458
2433 TGAACAATGATGTGGAATCTTAATAAAATTTA 2466
2459 AGAAATGATGAACTGACAGACATTCACAGAGTTA 2492

RESULT 12
US-09-992-598-56
Sequence 56, Application US/09992598
Patent No. 6956108
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR FILING DATE: 1998-07-09

Query Match 28.2%; Score 777.2; DB 3; Length 3462;
Best Local Similarity 59.8%; Pred. No. 3e-209;
Matches 1456; Conservative 0; Mismatches 948; Indels 30; Gaps 8;

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DB 77 TGAGAAATAAGTGTAAATCTTGAAATACATGAGACTCATGAAACATTTACAT 136
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DB 137 ATTTGTATGATTTGTTATGACGAGAGGGATGATCTCCAGAGCTCCAGAAAGGCA 196
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QY 225 AACCAAGCTTATGATATGCTCAGAACTACATGCTGAGCTTCAGGTCTTGACATGAG 284
DB 257 CACAACGACACTGAGATTATCTATTAACCTCTTTTCAACCTCCAGAGTTGAGATTTCA 316
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DB 317 TTCTGTCTCCAACTGAGAGTTTGAATTTATGCTATACGAATTCAGAGCTGAACTT 376
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DB 557 GAGTGGGCAAAATATACAAAATCAGATTTCCAGAAATTTGCTCATGCTATTAATATAC 616

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RESULT 13
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 / Patent No. 6972185
 / GENERAL INFORMATION:
 / APPLICANT: Ashkenazi, Avi J.
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan L.
 / APPLICANT: Ferrara, Napoleone
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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CURRENT APPLICATION NUMBER: US/09/989,735
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Matches 1456; Conservative 0; Mismatches 948; Indels 30; Gaps 8;

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RESULT 14
US-09-989-726-56
; Sequence 56, Application US/09989726
; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C60
CURRENT FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 28.2%; Score 777.2; DB 5; Length 3462;
Best Local Similarity 59.8%; Pred. No. 3e-209;
Matches 1456; Conservative 0; Mismatches 948; Indels 30; Gaps 8;

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RESULT 15
US-09-997-514-56

Sequence 56, Application US/09997514
Patent No. 7019116
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC46
CURRENT APPLICATION NUMBER: US/09/997,514
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match      28.2%; Score 777.2; DB 5; Length 3462;
Best Local Similarity 59.8%; Pred. No. 3e-209;
Matches 1456; Conservative 0; Mismatches 948; Indels 30; Gaps 8;

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DB 137 ATTTGTAGTATGTTATATGACAGAGAGGTGATGCTCCAGAGCTGCCAGAAAGAGGA 196
QY 165 ATTTCAGTAGCAAGTCAAAAAGAGCTTTATATCATGTTCCAAAAGACTACCGCTGA 224
DB 197 ACTGATGACCAACTGCTCCAAACATGCTCTTAAGAAAGGTTCCCGCAGACTGACCCACG 256
QY 225 AACCAAGCTTAGATATGCTCAGAACTACATCGCTGAGCTTCAGGTCTTGACATGAG 284

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 Qy 1899 GCCCTGTATCTCAGAGATGTTGTCAGTGAAGCCAGACTCGCGCAGGGCCAGGAACAT 1958
 Db 1919 GCCCTGTATCTCAGAGATGTCAGTGAATGCAATGCAACAAACATGGCAAGGGTTAGGAAAC 1978
 Qy 1959 ACCCTTAGAGACCTTCCAAAGAACCTCCAGTTTCAATGCTTTTATTTCAATATGAGACA 2018
 Db 1979 AACCCAGAACCACTCAAGAGAAATGTCCGATTCACAGCATTTATTTCAATACAGTGAACA 2038
 Qy 2019 TGATTTCTGCTGGGGAAGAAATGTTGTACTTAACCTAGAAAAAGAGA-----TAT 2072
 Db 2039 TGATTTCTGCTGGGGAAGAAATGTAATGATCCCAATCTAGAGAGAAAGATGTTCTAT 2098
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 Qy 2373 ACGTGGGCTTTTGGGGCTTAATATAGAGCGGCTTTTATATGAATTAACACTAGTCAAC 2432
 Db 2399 ATGTGGGCTTTTCTGGGCAAACTTTCAGAGCTGCTATTAATGTTAATGTTAGCCACAG 2458

Qy 2433 TGAAAAAATGATGTGAATCTTAAAAAATTTA 2466
 Db 2459 AGAAATGTATGAACCTGCAGACATTCACAGAGTTA 2492
 Search completed: June 5, 2006, 02:47:52
 Job time : 536 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 2, 2006, 22:53:23 ; Search time 157 Seconds
(without alignments)
4689.888 Million cell updates/sec

Title: US-10-732-796a-12

Perfect score: 4154

Sequence: 1 MTKDKRPIVSKFHFVCLMI.....IRAFNMKLTIVTENNDVKS 796

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_crembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4149	99.9	796	1	TLR6_HUMAN
2	3374	81.2	796	1	O59H16_PIG
3	3361	80.9	796	2	O76L23_PIG
4	3315	79.8	793	2	O704V6_BOVIN
5	3306	79.6	793	2	O706D2_BOVIN
6	3147.5	75.8	806	2	O6P690_RAT
7	3144.5	75.7	795	1	TLR6_MOUSE
8	3144.5	75.7	806	2	O3UV88_MOUSE
9	3143.5	75.7	806	2	O7TPC5_MOUSE
10	2830	68.1	786	1	TLR1_HUMAN
11	2830	68.1	786	2	O32MK3_HUMAN
12	2829	68.1	786	2	O32MK4_HUMAN
13	2828	68.1	786	2	O5FWG5_HUMAN
14	2817	67.8	796	2	O6F164_HUMAN
15	2654.5	63.9	796	2	O4UDR7_PIG
16	2654.5	63.9	796	2	O59H19_PIG
17	2525	60.8	795	1	TLR1_MOUSE
18	2468	59.4	727	2	O6A0E8_MOUSE
19	2400	57.8	727	2	O6GV21_BOVIN
20	2322	55.9	480	2	O2NKL3_HUMAN
21	1967	47.4	818	2	O5WA51_HUMAN
22	1965	47.3	818	2	O5Y1H8_CHICK
23	1905.5	45.9	811	2	O5Y1H8_CHICK
24	1902.5	45.8	811	1	TLR10_HUMAN
25	1899.5	45.7	811	2	O32MI8_HUMAN
26	1896.5	45.7	811	2	O32MI7_HUMAN
27	1850.5	44.5	811	2	O4UDR6_PIG
28	1847.5	44.5	811	2	O59H15_PIG
29	1838	44.2	812	2	O6GV17_BOVIN
30	1421	34.2	389	2	O8C1X4_CRIGR
31	1246.5	30.0	812	2	O5H727_FUGRU

32	1227	29.5	789	2	O4RZC3_TETNG	O4RZC3 tetradon n
33	1050	25.3	227	2	O56GY4_BOVIN	O56GY4 bos taurus
34	1050	25.3	227	2	O56GZ4_SHEEP	O56GZ4 ovis aries
35	1043.5	25.1	258	2	O3BR20_BOVIN	O3BR20 bos taurus
36	963.5	23.2	784	1	TLR2_MOUSE	O9QU97 mus musculus
37	963.5	23.2	784	2	O3U400_MOUSE	O3U400 mus musculus
38	963.5	23.2	784	2	O811T5_MOUSE	O811T5 mus musculus
39	962.5	23.2	784	2	O8K3D9_MOUSE	O8K3D9 mus musculus
40	951.5	22.9	784	2	O6YGU2_RAT	O6YGU2 rattus norv
41	946	22.8	784	1	TLR2_HUMAN	O60503 homo sapien
42	945.5	22.8	785	2	O76L24_PIG	O76L24 sus scrofa
43	943.5	22.7	784	1	TLR2_CRIGR	O9X1F8 cricetus
44	943.5	22.7	785	2	O59H18_PIG	O59H18 sus scrofa
45	940.5	22.6	785	2	O6TN21_PIG	O6TN21 sus scrofa

ALIGNMENTS

RESULT 1
TLR6_HUMAN STANDARD, PRT, 796 AA.
AC Q9Y2C9;
DT 31-JAN-2002, integrated into UniprotKB/Swiss-Prot.
DT 01-NOV-1999, sequence version 1.
DT 07-MAR-2006, entry version 42.
DE Toll-like receptor 6 precursor.
GN Name=TLR6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Placenta;
RX MEDLINE=99250250; PubMed=10231569; DOI=10.1016/S0378-1119(199)00098-0;
RA Takeuchi O., Kawai T., Sanjo H., Copeland N.G., Gilbert D.J.,
RT Jenkins N.A., Takeda K., Akira S.;
RT "TLR6: a novel member of an expanding Toll-like receptor family.";
RL Gene 231:59-65(1999).
RN [2]
RP FUNCTION.
RX MEDLINE=21334385; PubMed=11441107;
RA Bulut Y., Faure B., Thomas L., Equils O., Arditi M.;
RT "Cooperation of Toll-like receptor 2 and 6 for cellular activation by
soluble tuberculosis factor and Borrelia burgdorferi outer surface
protein A lipoprotein: role of Toll-interacting protein and Il-1
receptor signaling molecules in Toll-like receptor 2 signaling.";
RL J. Immunol. 167:987-994(2001).
CC -!- FUNCTION: Participates in the innate immune response to Gram-
positive bacteria and fungi. Acts via MyD88 and TRAF6, leading to
NF-kappa-B activation, cytokine secretion and the inflammatory
response. Recognizes mycoplasma macrophage-activating
lipopeptide-2kD (MALP-2), soluble tuberculosis factor (SFP),
phenol-soluble modulin (PSM) and B.burgdorferi outer surface
protein A lipoprotein (Ospa-L) cooperatively with TLR2.
CC -!- SUBUNIT: Binds TLR2 via their respective extracellular domains.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
phagosomes (By similarity).
CC -!- TISSUE SPECIFICITY: Detected in monocytes, CD11c+ immature
dendritic cells, plasmacytoid pre-dendritic cells and dermal
microvessel endothelial cells.
CC -!- SIMILARITY: Belongs to the Toll-like receptor family.
CC -!- SIMILARITY: Contains 13 IRR (leucine-rich) repeats.
CC -!- SIMILARITY: Contains 1 TIR domain.
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DR EMBL, AB020807; BAAV7631.1; -, mRNA.
DR HSPB, Q15399; 1FVY.

DR SMR; Q9Y2C9; 630-786.
 DR Ensembl; ENSG00000174130; Homo sapiens.
 DR HGNC; HGNC:16711; TLR6.
 DR MIM; 605403; gene.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0016020; C:membrane; ISS.
 DR GO; GO:0045335; C:phagocytic vesicle; ISS.
 DR GO; GO:0008034; F:lipoprotein binding; ISS.
 DR GO; GO:0042888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; NAS.
 DR GO; GO:0042742; P:defense response to bacteria; TAS.
 DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR GO; GO:0045064; P:macrophage activation; ISS.
 DR GO; GO:0045410; P:positive regulation of interleukin-12 biosyn. . .; ISS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR GO; GO:0042088; P:T-helper 1 type immune response; IC.
 DR InterPro; IPR004075; IL1_rcpt_1.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_C.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00560; LRR_1; 8.
 DR Pfam; PF01463; LRRCT; 1.
 DR PRINTS; PR01537; INTRIKRI1.F.
 DR PRINTS; PR00019; LEURICR1.F.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 DR Glycoprotein; Immune response; Inflammatory response; Innate immunity;
 KW Leucine-rich repeat; Membrane; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 31 Potential.
 FT CHAIN 32 796 TOLL-like receptor 6.
 FT FT 32 586 /FTid=PRO_0000034731.
 FT TRANSMEM 587 607 Extracellular (Potential).
 FT TOPO_DOM 608 796 Potential.
 FT REPEAT 51 74 Cyttoplasmic (Potential).
 FT REPEAT 75 98 LRR 1.
 FT REPEAT 100 120 LRR 2.
 FT REPEAT 121 144 LRR 3.
 FT REPEAT 158 175 LRR 4.
 FT REPEAT 176 201 LRR 5.
 FT REPEAT 222 248 LRR 6.
 FT REPEAT 222 248 LRR 7.
 FT REPEAT 376 400 LRR 8.
 FT REPEAT 402 428 LRR 9.
 FT REPEAT 430 447 LRR 10.
 FT REPEAT 449 472 LRR 11.
 FT REPEAT 474 496 LRR 12.
 FT REPEAT 498 517 LRR 13.
 FT DOMAIN 640 784 TIR.
 FT CARBOHYD 144 144 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 186 186 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 214 214 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 253 253 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 285 285 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 359 359 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 423 423 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 434 434 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 583 583 N-linked (GlcNAc . . .) (Potential).
 SQ SEQUENCE 796 AA; 91890 MW; 35CBAEC05BFBABD CRC64;

Query Match 99.9%; Score 4149; DB 1; Length 796;
 Best Local Similarity 99.9%; Pred. No. 8e-251;
 Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKKEPIYKSHFPCVMIITIVGTRIQPSDGNFPAIDKSKRGLIHVPKDLPLKTKYLDWS 60
 DB 1 MKKKEPIYKSHFPCVMIITIVGTRIQPSDGNFPAIDKSKRGLIHVPKDLPLKTKYLDWS 60

QY 61 QNYIAELQVSDMSFLSELTVLRLSHNRIQLDLSVFFKNODLELYLDSSHNOLOKISCHPI 120
 DB 61 QNYIAELQVSDMSFLSELTVLRLSHNRIQLDLSVFFKNODLELYLDSSHNOLOKISCHPI 120
 QY 121 VSPFRLDLSFNDPFLALPCKEFGNLSQLNPLGLSAMLQKLDLPIAHILHLSYLLDLRN 180
 DB 121 VSPFRLDLSFNDPFLALPCKEFGNLSQLNPLGLSAMLQKLDLPIAHILHLSYLLDLRN 180
 QY 181 YYIKENETESLIQINAKTLHLVFPHTSLFAIQVNI SVNTLGLQDLTNIKLNDNCQVFIK 240
 DB 181 YYIKENETESLIQINAKTLHLVFPHTSLFAIQVNI SVNTLGLQDLTNIKLNDNCQVFIK 240
 QY 241 FLSELTRGSLTNFTLNHIETTKVCLVRFQPLMPKPEYENIYNLTITISIREDEFTYS 300
 DB 241 FLSELTRGSLTNFTLNHIETTKVCLVRFQPLMPKPEYENIYNLTITISIREDEFTYS 300
 QY 301 KTLTKALTIETHTNOVPLFSOTALYTVSENNIMMLTISDPFTIHMCPHAPSTFKPLNF 360
 DB 301 KTLTKALTIETHTNOVPLFSOTALYTVSENNIMMLTISDPFTIHMCPHAPSTFKPLNF 360
 QY 361 TONVFTDSIFPKCSTLVLETLILQKGLKDLFVGLMTKDPSELILDVSMNSLSGRH 420
 DB 361 TONVFTDSIFPKCSTLVLETLILQKGLKDLFVGLMTKDPSELILDVSMNSLSGRH 420
 QY 421 KENCTWVESIVLNLSNMLTDSVFRCLPPIKVLDSHNKIKSVKQVVLKALQELNV 480
 DB 421 KENCTWVESIVLNLSNMLTDSVFRCLPPIKVLDSHNKIKSVKQVVLKALQELNV 480
 QY 481 AFNSLTDLPGGSGSSSVLLIIDHNSVSPADFPQSCQKRSIKAGNPFQCCELREF 540
 DB 481 AFNSLTDLPGGSGSSSVLLIIDHNSVSPADFPQSCQKRSIKAGNPFQCCELREF 540
 QY 541 VKNIDQVSSEVLEGPDSYKCDYPSYKSGPLKDFHMSLSCNTLLIVTIGATMLVLAV 600
 DB 541 VKNIDQVSSEVLEGPDSYKCDYPSYKSGPLKDFHMSLSCNTLLIVTIGATMLVLAV 600
 QY 601 TVTSICILYLDLPWYIRMYCQWOTRRRARNIPLELQNLDPHAFISSEHDSAMVSEL 660
 DB 601 TVTSICILYLDLPWYIRMYCQWOTRRRARNIPLELQNLDPHAFISSEHDSAMVSEL 660
 QY 661 VPLYEKEDIQICLHRNFVPGKSIYENIINCIEKSYKSI FVLSPPVQSEMCHELYPEAH 720
 DB 661 VPLYEKEDIQICLHRNFVPGKSIYENIINCIEKSYKSI FVLSPPVQSEMCHELYPEAH 720
 QY 721 HNLFFHGSNNLILILLEPIPNKHYKUKALMTORTYLOMPKSKRGIFMANIRAA 780
 DB 721 HNLFFHGSNNLILILLEPIPNKHYKUKALMTORTYLOMPKSKRGIFMANIRAA 780
 QY 781 FNMKLTLYTENNDVKS 796
 DB 781 FNMKLTLYTENNDVKS 796

RESULT 2
 Q59HI6_PIG PRELIMINARY; PRT; 796 AA.
 AC Q59HI6;
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 26-APR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE TOLL-like receptor 6.
 GN Name=TLR6;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 NCBI_TaxID=9823;
 OX NCBI_TaxID=9823;
 RN NUCLEOTIDE SEQUENCE.
 RP Shinkai H., Uenishi H.;
 RA "Coding sequence of porcine TLR6";
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 [2]

RP NUCLEOTIDE SEQUENCE.
RA Shinkai H., Uenishi H.;
RT "Nucleotide sequence of porcine genomic region containing TLR1, TLR6
RT and TLR10";
RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
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EMBL, AB208698, BAD91801.1, -, Genomic DNA.
EMBL, AB210286, BAD93713.1, -, Genomic DNA.
DR SMR, Q59H16, 630-785.
DR GO, GO:0016020, C:membrane; IEA.
DR GO, GO:0004888, F:transmembrane receptor activity; IEA.
DR InterPro, IPR004075, IL1_rcpt_1.
DR InterPro, IPR001611, LRR.
DR InterPro, IPR004483, LRR_C.
DR InterPro, IPR003591, LRR_Typ.
DR InterPro, IPR000157, TIR.
DR Pfam, PF00560, LRR_1, 7.
DR Pfam, PF01463, LRRCT, 1.
DR Pfam, PF01582, TIR, 1.
DR PRINTS, PR01537, INTRLNRI1.F.
DR PRINTS, PR00019, LEURICHRPT.
DR SMART, SM00082, LRRCT, 1.
DR SMART, SM00255, TIR, 1.
DR PROSITE, PS50104, TIR, 1.
KM Receptor.
SQ SEQUENCE 796 AA; 91460 MW; 8CE2A2375606CA55 CRC64;

Query Match 81.2%; Score 3374; DB 2; Length 796;
Best Local Similarity 79.4%; Pred. No. 2, 4e-202;
Matches 632; Conservative 77; Mismatches 87; Indels 0; Gaps 0;

QY 1 MTKDKEPIVKSFFHYCLMIITIVGTRIQPSDGNFAVDKSKRGILHVPKDLPIKTVLDM 60
DB 1 MSKDKEPIVTSISHSYVMTLVWGTLIQFSESEFVVDKSKIGLTRVPKDLPTQTVL 60
QY 61 QNYIAELQVSDMSFUSELTVLRSLSHNRITQLDLVFKENQDLEVIYDLISHNOLOKISCH 120
DB 61 QNYIAELHSDISFISQTLVRLSQNRMQCLDISVFKFNQDLEVIYDLISHNOLOKISCH 120
QY 121 VSFRLHDSFNDFKALPICKERGNLSQNLFLGLSAMKLOKDLPLIAHMLSYILLDLN 180
DB 121 TSKRLHDSFNDFKALPICKERGNLTQNLFLGLSATKLOQDLPLIAHMLSCILLDLN 180
QY 181 YYIKENETESIQILNAKTLHLVHFPTSLPAIVNISVNTLGLQOLTNIKLNDNCQVPIK 240
DB 181 YYMKENKESIQILNMTKKLHLVFHNSPFSVQVNISVSKVGLQLANIKLSDNCQVPIK 240
QY 241 FUSELTRGSTLINFNLNIETWKCLVRFQFLMPKPEVYININVTITESTIREDFYIS 300
DB 241 FLELETRQPTLINFNLNIETWKCLVGIQFLMPKPEVYISINVTITESTIREDFYIY 300
QY 301 KTTLKALTIENHTNQVLFESOTALTVPSENNIMMLTISDPFIHMLCPHASTREPLNF 360
DB 301 ETTLKGVKTIENHTKRVFLFSQTLRVFSQVNIIRMLTADHFIHMLCQVSTENPLNF 360
QY 361 TQNVFTDSIFPKCSTLVKLETLILQKNGIKDLFKVGLMTKMDPSLEILDVSNWSIESGRH 420
DB 361 TQNVFTDSVFQCKTLARLETLILQKNGIKDLFKVGLMTKMDPSLEILDVSNWSIESGRH 420
QY 421 KENCWVSGSIYVLANISSNMULTSVRCPLPRIKVLDLHSHNRISIPKVAHLEALQELNV 480
DB 421 GENCWVSGSIYVLANISSNLTDSVRCPLPRIKVLDLHSHNRISIPKVAHLEALQELNV 480
QY 481 AFNSITLDPGCGSFSLSVLILIDHNSVSHPSADFPQSCQKMSIRAGDNPFOCTCELARF 540
DB 481 ASNSLAHLPGCGSFSLSITLIDHNSISNPSADFPQSCQKISIRAGDNPFOCTCELARF 540
QY 541 VKNIDQVSSVEVLGMPDSYKCDYPESYRSGPLKDFHMSLSCNITLLITVITATMLVLAV 600
DB 541 IQSLQVSSDVVSWPDSYECEYPESYKGTLLKDFVSELSCNTALLITVITATMLVLAV 600

QY 601 TWTSLCIVLDFWYLRMVCOMQOTRRRARNPLEELQRLQFHAISYSEHDSAWKSEL 660
DB 601 TWTGLCVFDFLPMYIRMLCOMQOTRRRARNPVLEELQRLQFHAISYSEHDSAWKSEL 660
QY 661 VPLEKEDIQICLHERNPVPGKSIYENIINCIEKYSKISFVLSPNFVQSEWCHYELYPFH 720
DB 661 VPLEKEGKICILHERNPVPGKSIYENIINCIEKYSKISFVLSPNFVQSEWCHYELYPFH 720
QY 721 HNLFHEGSGNNLILILPELPONSIPNKYHKALKMTORTYLOMPREKSKRGFLMANIRAA 780
DB 721 HNLFHEGSGNNLILILPELPONSIPNKYHKALKMAORTYLEWPREKSKRGFLMANIRAA 780
QY 781 FNMKRLTVTENNDVKS 796
DB 781 FNIKXKLVAEEDVKT 796

RESULT 3
ID 076L23 PIG PRELIMINARY; PRT; 796 AA.
AC 076L23;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Toll-like receptor 6.
GN Name=TLR-6;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22948431; PubMed=14585198; DOI=10.1089/107999003322485080;
RA Muneta Y., Uenishi H., Kikuma R., Yoshihara K., Shimoji Y.,
RA Yamamoto R., Hamashima N., Yokomizo Y., Mori Y.;
RT "Porcine TLR2 and TLR6: identification and their involvement in
RT Mycoplasma hyopneumoniae infection."
RL J. Interferon Cytokine Res. 23:583-590(2003).
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CC -----
EMBL, AB065936, BAC99317.1, -, mRNA.
DR SMR, Q76L23, 630-785.
DR GO, GO:0016020, C:membrane; IEA.
DR GO, GO:0004888, F:transmembrane receptor activity; IEA.
DR InterPro, IPR004075, IL1_rcpt_1.
DR InterPro, IPR001611, LRR.
DR InterPro, IPR000483, LRR_C.
DR InterPro, IPR003591, LRR_Typ.
DR InterPro, IPR000157, TIR.
DR Pfam, PF00560, LRR_1, 7.
DR Pfam, PF01463, LRRCT, 1.
DR Pfam, PF01582, TIR, 1.
DR PRINTS, PR01537, INTRLNRI1.F.
DR PRINTS, PR00019, LEURICHRPT.
DR SMART, SM00082, LRRCT, 1.
DR SMART, SM00255, TIR, 1.
DR PROSITE, PS50104, TIR, 1.
KM Receptor.
SQ SEQUENCE 796 AA; 91414 MW; 36C489D2CC339F81 CRC64;

Query Match 80.9%; Score 3361; DB 2; Length 796;
Best Local Similarity 79.1%; Pred. No. 1, 6e-201;
Matches 630; Conservative 77; Mismatches 89; Indels 0; Gaps 0;

QY 1 MTKDKEPIVKSFFHYCLMIITIVGTRIQPSDGNFAVDKSKRGILHVPKDLPIKTVLDM 60
DB 1 MTKDKEPIVTSISHSYVMTLVWGTLIQFSESEFVVDKSKIGLTRVPKDLPTQTVL 60
QY 61 QNYIAELQVSDMSFUSELTVLRSLSHNRITQLDLVFKENQDLEVIYDLISHNOLOKISCH 120

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Db      61 QNFTEHLSDISFSLQTLVRLSQNRMOCLDISVFKENODLEYLDLSHNQLOTLICHP1 120
Qy      121 VSPFRLDLSFNDPKALPICKERGNLSQNLFLGLSAMKLOKLDLPIALHLISYILLDRN 180
Db      121 TSLKHLDSFNDPKALPICKERGNLTQANFLGLSATKLOQDLPLIAHLHLISCLLDLDR 180
Qy      181 YYIKENETESLOILNAKTLHLVFPHTSLPAIOVNI SVNTLGGLOLTNIKLNDNCQVFLK 240
Db      181 YYMKENKESLOILNTEKHLVFPHTSPFSVQVNI SVKSGLOLANIKLGDNCQVFLT 240
Qy      241 FLSELTGSLTLNFTLNHIEFTWKLVAVFOFLMKPEVYININVTLLIESREEDFTYS 300
Db      241 FLEELTQGPRTLNFPLNHVEITWKLVGFOFLMKPEVYISINVTLLIESIDEDFTLY 300
Qy      301 KTLTKALTEHTNNOVFLFSOTALTVESENNIMLTSDPFIHMLCPHASTKFLNLF 360
Db      301 ETLTKGVKTEHTTKVFI FSQTLAVFSDMNIIMLTADTFIIMLCQVSTNFTNLF 360
Qy      361 TQNVFTDSIFEKCSLTVKLETLILQKNGKLDL FKVGLMTKMPSEILDVSNLSGSRH 420
Db      361 TQNVFTDSVFQCKTLARLETLILQKMKEDLFKISMTKMDLSLEILDVSSNSLEYDRH 420
Qy      421 KENCTWVESIYVNLSSNMLTDSVFRCLPPIKIVLDHSNKIKSVKQVYKLEALQELNV 480
Db      421 GENCTWVGSIYVNLSSNMLTDSVFRCLPPIKIVLDHSNIRISIPKDVANLEALQELNV 480
Qy      481 AFNLSLTDLPGGGSFSLSVLIIIDHNSVSHSPADFPQSCOKMRSIKAGDPQCTGELREF 540
Db      481 ASNSLAHLPGGGSFSLSLISIDVNSISNPSADFPQSCOKIRSLKAGNNPQCTGELNRF 540
Qy      541 VKNIDVSSSEVLBGMPSYKCDYPESYRGSPKDFHMSLSGNITLLIYTTIGATMLVLAV 600
Db      541 IQSGQVSSDVVBSMPDSECEYSGYGTLLKDFRVSLSGNTALLIYTTIGATMLVL 600
Qy      601 TVTSLCTYLDLPWYLRWVQWQTQTRRRANIPLEELQRLQTHAITSYSEHDSAVYKSEL 660
Db      601 TMTGCVYFDLPWYLRWVQWQTQTRRRANIPLEELQRLQTHAITSYSEHDSAVYKSEL 660
Qy      661 VPYLEKEIOICLHERNFVPGKSIYVENIINCIEKSYKSI FVLSNPNVQSEWCHYELVFAH 720
Db      661 VPCLKEBGKICLHERNFVPGKSIYVENIINCIEKSYKSI FVLSNPNVQSEWCHYELVFAH 720
Qy      721 HNLFHSGSNLTLILLEPIQNSIPNKYHKLKALMTORTYLOMPKESKRGFLFWANIRAA 780
Db      721 HNLFHSGSDNLTLLILDDPIQNSIPGKYHKLKALMAQRTYLEMPKESKRGFWANIRAA 780
Qy      781 FNMKLTIVTENNDVKS 796
Db      781 FNIKKLVAEEDDVKT 796

RESULT 4
ID Q704V6_BOVIN PRELIMINARY; ERT; 793 AA.
AC Q704V6;
DT 05-JUN-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUN-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Toll-like receptor 6.
GN Name=tlr6;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yang Y., Weikard R., Zerbe H., Seyfert H.M.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AJ620670; CAJ6197.1; -; Genomic DNA.
DR SMR; Q704V6; 630-789.
DR Ensemble; ENSBTFAG000000014031; Bos taurus.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR004075; IIL_1.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_C.
DR InterPro; IPR003591; LRR_TYP.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR_1; 7.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR01537; INTRLNRI1F.
DR PRINTS; PR000439; LEURICRPT.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS0104; TIR; 1.
DR Receptor.
SQ SEQUENCE 793 AA; 90927 MW; C11C26099F8E3668 CRC64;

Query Match          79.8%; Score 3315; DB 2; Length 793;
Best Local Similarity 79.5%; Pred. No. 1.2e-198;
Matches 625; Conservative 73; Mismatches 86; Indels 2; Gaps 2;

1  MTKDEPIVKSFFHFCMLIIIVGTRIQPSDGNFVADSKRGILHVPKDLPTKVLDMS 60
Db  1  MIKDKESPTRCHFYIALVFGTIIQPSDSEFVDMKSLIHVPKDLPTKVLDLS 60
Qy  61  QNYIAELQVSDMSFLSELTVRLSHNRIQILDVSVKKNODELYLDLSHNQLOKISCHPI 120
Db  61  QNNISELHLSDISFSLGRLVRLSHNRIOGLDISIFKFNHDELYLDLSHNQLOKISCHPI 120
Qy  121 -VSFRHLDSFNDPKALPICKERGNLSQNLFLGLSAMKLOKLDLPIALHLISYILLDR 179
Db  121 TTTLKHLDLSFNDPKALPICKERGNLTQANFLGLSATKLOQDLPLIAHLHLISCLLDLDR 180
Qy  180 NYIYIKENETESLOILNAKTLHLVFPHTSLPAIOVNI SVNTLGGLOLTNIKLNDNCQVFI 239
Db  181 D-YMKENKESLOILNTEKHLVFPHTSPFSVQVNI SVKSGLOLANIKLGDNCQVFLT 239
Qy  240 KFLSELTRGSLTLNFTLNHIEFTWKLVAVFOFLMKPEVYININVTLLIESIREEDFTY 299
Db  240 KFLSGLTGPTLNFPLNHVEITWKLVGFOFLMKPEVYISINVTLLIESIDEEVFTY 299
Qy  300 SKTTLKALTIEHTNNOVFLFSOTALTVESENNIMLTSDPFIHMLCPHASTKFLNLF 359
Db  300 YKTLKALKIEHTNKVFI FSQTLAVFSENNIMLTSDPFIHMLCPHASTKFLNLF 359
Qy  360 FTQNVFTDSIFEKCSLTVKLETLILQKNGKLDL FKVGLMTKMPSEILDVSNLSGSRH 419
Db  360 FTQNSFTDSVFQCKTLARLETLILQKMKEDLFKISMTKMDLSLEILDVSSNSLEYDR 419
Qy  420 HKNCTWVESIYVNLSSNMLTDSVFRCLPPIKIVLDHSNKIKSVKQVYKLEALQELNV 479
Db  420 SNNGNSWVGSIYVNLSSNMLTDSVFRCLPPIKIVLDHNNIRISIPROVGLTLELOELN 479
Qy  480 VAFNLSLTDLPGGGSFSLSVLIIIDHNSVSHSPADFPQSCOKMRSIKAGDPQCTGELREF 539
Db  480 LASNSLAHLPGGGSFSLSLISIDVNSISNPSADFPQSCOKIRSLKAGNNPQCTGELNRF 539
Qy  540 FVKNIDVSSSEVLBGMPSYKCDYPESYRGSPKDFHMSLSGNITLLIYTTIGATMLVLVA 599
Db  540 FIQSGQVSSDVVBSMPDSECEYSGYGTLLKDFRVSLSGNTALLIYTTIGATMLVLVA 599
Qy  600 VVTWTSICTYLDLPWYLRWVQWQTQTRRRANIPLEELQRLQTHAITSYSEHDSAVYKSE 659
Db  600 VAVTVLCTYLDLPWYLRWVQWQTQTRRRANIPLEELQRLQTHAITSYSEHDSAVYKSE 659
Qy  660 LVPLYLEKEDIOICLHERNFVPGKSIYVENIINCIEKSYKSI FVLSNPNVQSEWCHYELVFA 719
Db  660 LIPNLEKEDIRICLHERNFVPGKSIYVENIINCIEKSYKSI FVLSNPNVQSEWCHYELVFA 719

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QY	720	HNNLHEGSSNNILILILEEPIPNISINPKYHKU.KALMTORTYU.COMPEKSKRG.FWMNIRA	779
Db	720	HNNLHEGSSNNILILILDEPIPOISIPSSYHKU.KALMAQRTYU.LSEWPEKSKRG.FWMNIRA	779
QY	780	AFNMKL 785	
Db	780	SINIKL 785	
RESULT 5			
ID	Q706D2	BOVIN	PRELIMINARY; PRT; 793 AA.
AC	Q706D2		
DT	05-JUN-2004		integrated into UniProtKB/TrEMBL.
DT	05-JUL-2004		sequence version 1.
DT	07-FEB-2006		entry version 12.
DE	Toll-like receptor 6.		
GN	Name=tlr6;		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;		
OC	Bos; Bovidae; Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RN	(1)		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Mammary gland.		
RA	Yang W., Weikard R., Zeirde H., Seyfert H.M.,		
RL	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.		
RN	(2)		
RP	NUCLEOTIDE SEQUENCE.		
RA	Wierling D.;		
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.		
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CC	-----		
DR	EMBL; AJ618974; CAF02015.1; -; mRNA.		
DR	EMBL; AY487803; AAY40896.1; -; mRNA.		
DR	Ensembl; ENSBTAG00000014031; Bos taurus.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0004888; F:transmembrane receptor activity; IEA.		
DR	InterPro; IPR004075; IL1_rcpt_1.		
DR	InterPro; IPR001611; LRR_		
DR	InterPro; IPR000483; LRR_C.		
DR	InterPro; IPR003591; LRR_Typ.		
DR	InterPro; IPR000157; TIR.		
DR	Pfam; PF00560; LRR_1; 7.		
DR	Pfam; PF01463; LRRCT; 1.		
DR	Pfam; PF01582; TIR; 1.		
DR	PRINTS; PRO1537; INTRLNKINR.F		
DR	PRINTS; PRO0019; LEURICHRPT.		
DR	SMART; SM00082; LRRCT; 1.		
DR	SMART; SM00255; TIR; 1.		
DR	PROSITE; PSS0104; TIR; 1.		
DR	Receptor		
QY	SEQUENCE	793 AA, 90927 MW; D52422389B09F28F CRC64;	
Query Match 79.6%; Score 3306; DB 2; Length 793;			
Best Local Similarity 79.4%; Pred. No. 4,3e-198;			
Matches 624; Conservative 73; Mismatches 87; Indels 2; Gaps 2			
QY	1	MTKDKDEPIVSKSHFPCMLIIYIGTRQFSDNGNEFAVDKSKRGILNHPKDLPLTKYLDMS	60
Db	1	MTKDKESPIRSHCFYIYIVAVLFGTIIQFSDESEFVDMSTSLIHVPKDLPPPTKYLDIS	60
QY	61	QNYIAELQVDSMFSISELTIVRLSHNRIGLDLVEFKFNQDLEYLDLSHNQLOKISCHPI	120
Db	61	QNNISELHSDISPISSGLKVLRLSHNRIGGLDIPKFNHDELYLDLSHNQLOKISCHPI	120
QY	121	VSPFHLDISFNDKALPICKRFGNLSQINFLGLSAMKLOKLDLPIALHLSTYILLDR	179
Db	121	VSPFHLDISFNDKALPICKRFGNLSQINFLGLSAMKLOKLDLPIALHLSTYILLDR	179

Db	121	ITTLKHLDDLSPDFPALP	1	CKEFGULQUNFGLSATKQDQDLPLIALHLHLSCLILDD	180
Qy	180	NYVKEKETESLOIIMAKTLHLVHPPTSLFAIQVNI	SVNTLGCLOJTNIKLANDNCQVFI	239	
Db	181	D-YMKENKESQIQUINTKTLHLVHPHNSFFSVQVD	ISGNSLACLQLTNKLANDYNCQVLL	239	
Qy	240	KFLSLTRGSLTANLTNHHIETTWKCIARVPOFWMPK	PVEYINIVLTIIESIREDFTY	239	
Db	240	KFLSGLTGPTLNTLNLHVTWCKLVKVFQFLWPKPL	EYINIVLTIVESIDEDEFTY	239	
Qy	300	SKTTLKALTIIEHTIQVLFESQTAIYTVFSENNIML	LTISDPFIHMLCPHAPSTFEFLN	355	
Db	300	YKTLTKALKIEHTIKVFI	FSQTAIYTVFSENNIMLTI	SDRFIHMLCPQESTKFLN	355
Qy	360	FTQNVFTDSIFEKSCSTLYKLETLILQKNGKLDL	FKVGLMTKMPSLIIDLVSNSLESGR	419	
Db	360	FTQNSFTDSVFQNCOTLARLETLILQKNEIKLDL	PKTSLMTKMLSIETLIDVSNSLEYDR	419	
Qy	420	HKENQWVESIVVNLSSNMLTDSVPRCLPRIKVL	LDLHNSKIKSVPKQVVKLEALOELN	479	
Db	420	SNGCSWGSIVVNLSSNALTDSVPRCLPRIKVL	DLNNRIRSPKQVTGLETQELN	479	
Qy	480	VAFNSLTLPQGGSPSSLSVLIIHNSVSHPADP	FSQCKRSTKAGDNPQCTCELR	539	
Db	480	IANSLSLHPPGGCFSSLSILIIENNSISNPADP	FSQCKRSLRAGANNPQSCCELR	539	
Qy	540	FVKNIQVSVSELTLEGMPDPSYKCDPESYKSGP	LKDFHMSLSCNTITLLITVIGATMLVLA	599	
Db	540	FIQSGQVSVSDVBEWBPESYKCDPESYKGTPL	KQFQVSELSCNTMLLIITIVVGLVLA	599	
Qy	600	VTVTSLCTIYLDLPWLYRMVCOMTQRRRARNI	PLELOENLOPHAFISYSEHDSAVKSE	659	
Db	600	VAVTVLCIYLDLPWLYRMVCOMTQRRRARNP	LELOQTLPHAFISYSEHDSAVKNE	659	
Qy	660	LVPYLEKEDIQICHERNFVPEKSI	IVENINICIEKSYKSI	FIPLSPVQSEWCHYELVYA	719
Db	660	LIPLEKEDIQICHERNFVAKSIVENINICIEKSYKSI	PAVLSPEVQSEWCHYELVYA	719	
Qy	720	HHNLFHESNNMLIILLEPPI	PONSIPNKYHKLKALMTORTYQWPEKSKRGFLFMANIRA	779	
Db	720	HHNLFHESNNMLIILLDPI	PQYSIPSTHTKRLALMAQTYLEWPEKSKRGFLFMANIRA	779	
Qy	780	AFNMKL	785		
Db	780	SINIKL	785		
RESULT 6					
Qy	06P690	RAT	PRELIMINARY;	PRT;	806 AA.
Db	06P690	RAT	PRELIMINARY;	PRT;	806 AA.
Qy	05-JUL-2004	integrated info UniProtKB/TrEMBL.			
Db	05-JUL-2004	sequence version 1.			
Qy	07-FEB-2006	entry version 12.			
Db	07-FEB-2006	entry version 12.			
Qy	GN	Name=Trf6;			
Db	GN	Name=Trf6;			
Qy	OS	Rattus norvegicus (Rat).			
Db	OS	Rattus norvegicus (Rat).			
Qy	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Db	OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
Qy	OC	Muroidea; Muridae; Murinae; Rattus.			
Db	OC	Muroidea; Muridae; Murinae; Rattus.			
Qy	NCBI	TaxID=10116;			
Db	NCBI	TaxID=10116;			
Qy	NP	NUCLEOTIDE SEQUENCE.			
Db	NP	NUCLEOTIDE SEQUENCE.			
Qy	RC	MESELM=22388257;	PubMed=12477932;	DOI=10.1073/pnae.242603899;	
Db	RC	MESELM=22388257;	PubMed=12477932;	DOI=10.1073/pnae.242603899;	
Qy	RA	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
Db	RA	Klausner R.L., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,			
Qy	RA	Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,			
Db	RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
Qy	RA	Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
Db	RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
Qy	RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
Db	RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,			

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibb S.A.,
RA Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blikstein R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rotherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RA Director MGC Project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL, BC062390, AA062390.1; -, mRNA.
DR SMR, Q6P690, 641-796.
DR Ensembl, ENSRNOG0000002161, Rattus norvegicus.
DR GO, GO:0016020, C:membrane, IEA.
DR GO, GO:0004888, F:transmembrane receptor activity, IEA.
DR InterPro, IPR004075, IL1_rpt_1.
DR InterPro, IPR001611, LRR_1.
DR InterPro, IPR000483, LRR_C.
DR InterPro, IPR003591, LRR_Typ.
DR Pfam, PF00560, LRR_1, 8.
DR Pfam, PF01463, LRRCT, 1.
DR Pfam, PF01582, TIR, 1.
DR PRINTS, PRO1537, INTRLNRLP.
DR PRINTS, PRO0019, LEURICRPT.
DR SMART, SM00369, LRR_Typ, 1.
DR SMART, SM00082, LRRCT, 1.
DR SMART, SM00255, TIR, 1.
DR PROSITE, PS50104, TIR, 1.
KM Receptor.
SQ SEQUENCE 806 AA; 92567 MW; F157F9D6447DAF3A CRC64;
Query Match 75.8%; Score 3147.5; DB 2; Length 806;
Best Local Similarity 74.2%; Pred. No. 3.6e-188;
Matches 591; Conservative 91; Mismatches 113; Indels 1; Gaps 1;
QY 1 MTKDEPIYKSPHYVCLMIIIVGTRIQSPDGNFPAVDKSKRGLIHVPKOLPLKTKVLDMS 60
DB 12 MSQDEPIVESPHFVCTALIVGSMTQFDELESVDVSNKXULTHVPKDLSPTKSLISIS 71
QY 61 ONYIAELOVDMSFSELTVLRLSNRIQLDLSPKFNQDLEVDLISNOLOKISCHPI 120
DB 72 QNSISDLQMSDLSFSELRLVLSNRIQLDLSPKFNQDLEVDLISNOLOKISCHPI 131
QY 121 VSFRLDLSFNDPKALPICKEFGNLSQNLFLGLISAMKLOKLLPLAHHLVYLLDLRN 180
DB 132 VNLKRLDLSFNDPKALPICKEFGNLSQNLFLGLISAMKLOKLLPLAHHLVYLLDLRN 191
QY 181 YIKENETESQILNAKTLHLVPHPTSLFAIQVNSVNTLGLQLTNKLNDNCQVPIK 240
DB 192 YQIKGETESQILNPVNTNLVLFVHPSPSLPSVQVNSVNTLGLQLTNKLNDNCQVPIK 251
QY 241 FLSELTRSTLNLNLTNHTETWKCLVRFQFLMPDVEVYNTVNTTIESIREDFPM 300
DB 252 FLSELTRSTLNLNLTNHTETWKCLVRFQFLMPDVEVYNTVNTTIESIREDFPM 311
QY 301 KTKLALTEHTITNOVFLFSQALYTVFSENNIMMLTISDTPFIHMLCPHASTFEKFLNF 360
DB 312 ETVLKSLEKHEHTNOVFLFSQALYTVFSENNIMMLTISDTPFIHMLCPHASTFEKFLNF 371
QY 361 TQNVFTDSIFEKCSITLVKLETLILQKNGKDLFKVGLMTKDPMSLEILDVSNMSLESGRH 420

DB 372 TQNVFTDSIFEKCSITLVKLETLILQKNGKDLFKVGLMTKDPMSLEILDVSNMSLESGRH 431
QY 421 KENTCTVESITVNLNLSNMLTDSVFCRPPRIKYLDLSNRIKISYKQVVKLEALQELNV 480
DB 432 DRTCMASIRKVLNLSNMLTDSVFCRPPRIKYLDLSNRIKISYKQVVKLEALQELNV 491
QY 481 AFSNITDLPGCCSPSSLSVLIIDHNSVSPADFPQSCQKRSIAGNPPROCTCELEEF 540
DB 492 ASNFLTDLPGCGAFSSLSVLVIDHNSVSPADFPQSCQKRSIAGNPPROCTCELEEF 551
QY 541 VKNIDQVSEVLEGGPDSPKCDYSPESYSGSPDKDPHMSLSCNTLLIVTTGATVLYAV 600
DB 552 VKNIDQVSEVLEGGPDSPKCDYSPESYSGSPDKDPHMSLSCNTLLIVTTGATVLYAV 611
QY 601 TWTSLICLYLDLPWYLRNWCQMTQTRRARNPISLELQNLQFNAFISYSEHDSAVNKS 660
DB 612 IGASLCILYLDLPWYLRNWCQMTQTRRARNPISLELQNLQFNAFISYSEHDSAVNKS 671
QY 661 VPELEKEDIQICLHERNFVPGKSIYENIINCIEKYSKIFVLSNPFVQSEWCHIELYFAH 720
DB 672 LPNLEKDDIRVCLHERNFVPGKSIYENIINCIEKYSKIFVLSNPFVQSEWCHIELYFAH 731
QY 721 HNLFFHSGNNLILILEPIPNQSI PNKYHKLKALMTORTYLOMPKSKRGLFWANIRAA 780
DB 732 HNLFFHSGNNLILILEPIPNQSI PNKYHKLKALMTORTYLOMPKSKRGLFWANIRAA 791
QY 781 FNMKRLTLVTENNVDYKS 796
DB 792 FNMKRLTLVTENNVDYKS 806
RESULT 7
TIR6 MOUSE STANDARD; PRT; 795 AA.
ID TIR6 MOUSE
AC OE9EP9: Q9WT04; Integrated into UniProtKB/Swiss-Prot.
DT 31-JAN-2002, sequence version 2.
DT 07-MAR-2006, entry version 40.
DE Toll-like receptor 6 precursor.
GN Name=Tlr6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Embryo;
RX MEDLINE=99250250; PubMed=10231569; DOI=10.1016/S0378-1119(99)00098-0;
RA Takeuchi O., Kawai T., Sanjo H., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Takeda K., Akira S.,
RT "Tlr6: a novel member of an expanding Toll-like receptor family";
RL Gene 231:59-65(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA], AND MUTAGENESIS OF PRO-680.
RC STRAIN=Balb/c; TISSUE=Macrophage;
RX MEDLINE=2058581; PubMed=11095740; DOI=10.1073/pnas.250476497;
RA Ozinsky A., Underhill D.M., Fontenot J.D., Hajjar A.M., Smith K.D.,
RA Wilson C.B., Schroeder L., Aderem A.,
RT "The repertoire for pattern recognition of pathogens by the innate
RT immune system is defined by cooperation between Toll-like receptors";
RL Proc. Natl. Acad. Sci. U.S.A. 97:13766-13771(2000).
CC -!- FUNCTION: Participates in the innate immune response to Gram-
CC positive bacteria and fungi. Acts via MyD88 and TRAF6, leading to
CC NF-kappa-B activation, cytokine secretion and the inflammatory
CC response. Cooperates with TLR2 for the cellular activation (by
CC similarity).
CC -!- SUBUNIT: Binds TLR2 via their respective extracellular domains.
CC Binds MyD88 via their respective TIR domains (by similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
CC phagosomes.
CC -!- TISSUE SPECIFICITY: Detected in thymus, spleen, ovary and lung.
CC -!- SIMILARITY: Belongs to the Toll-like receptor family.

CC	-1- SIMILARITY: Contains 1 LRR leucine-rich repeats.
CC	-1- SIMILARITY: Contains 1 TIR domain.
CC	-----
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CC	Distributed under the Creative Commons Attribution-NoDerivs license
CC	-----
DR	EMBL; AB020806; BAA78632.1; ALT_INIT, mRNA.
DR	EMBL; AF314636; AAG38563.1; ALT_INIT; mRNA.
DR	HSSP; Q15399; 1FVY.
DR	SMR; Q9EPW9; 630-785.
DR	Ensembl; ENSMUSG00000051498; Mus musculus.
DR	MGI; MGI:1341296; Tir6.
DR	GO; GO:0016021; C:integral to membrane; TAS.
DR	GO; GO:0016020; C:membrane; ISS.
DR	GO; GO:0045335; C:phagocytic vesicle; ISS.
DR	GO; GO:0008034; F:lipo-protein binding; IMP.
DR	GO; GO:0004088; F:transmembrane receptor activity; ISS.
DR	GO; GO:0007280; P:activation of NF-kappaB-inducing kinase; ISS.
DR	GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR	GO; GO:0042116; P:macrophage activation; ISS.
DR	GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; NAS
DR	GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS
DR	GO; GO:0042088; P:T-helper 1 type immune response; IC.
DR	InterPro; IPR004075; Tir_tcrp_1.
DR	InterPro; IPR001611; LRR.
DR	InterPro; IPR000483; LRR_C.
DR	InterPro; IPR003591; LRR_TYP.
DR	InterPro; IPR000157; TIR.
DR	Pfam; PF00560; LRR_1; 6.
DR	Pfam; PF01463; LRRT; 1.
DR	Pfam; PF01582; TIR; 1.
DR	PRINTS; PR01537; INTRLNRI1F.
DR	PRINTS; PRO0019; LEURICRPT.
DR	SMART; SMO0369; LRR_TYP; 1.
DR	SMART; SMO0082; LRRT; 1.
DR	SMART; SMO0255; TIR; 1.
DR	PROSITE; PS50104; TIR; 1.
KW	Glycoprotein; Immune response; Inflammatory response; Innate immunity;
KW	Leucine-rich repeat; Membrane; Receptor; Repeat; Signal;
KW	Transmembrane.
FT	SIGNAL 1 27 Potential.
FT	CHAIN 28 795 Toll-like receptor 6.
FT	TOPO_DOM 28 584 /Ptm=PRO_0000034732.
FT	TRANSMEM 585 605 Extracellular (Potential).
FT	TOPO_DOM 606 795 Potential.
FT	REPEAT 32 51 Cytoplasmic (Potential).
FT	REPEAT 32 75 LRR 1.
FT	REPEAT 32 75 LRR 2.
FT	REPEAT 76 98 LRR 3.
FT	REPEAT 100 120 LRR 4.
FT	REPEAT 121 144 LRR 5.
FT	REPEAT 146 171 LRR 6.
FT	REPEAT 225 248 LRR 7.
FT	REPEAT 330 353 LRR 8.
FT	REPEAT 376 399 LRR 9.
FT	REPEAT 402 425 LRR 10.
FT	REPEAT 427 449 LRR 11.
FT	REPEAT 459 472 LRR 12.
FT	REPEAT 473 496 LRR 13.
FT	REPEAT 498 517 LRR 14.
FT	TIR.
FT	N-linked (GLCNAc. . .) (Potential).
FT	N-linked (GLCNAc. . .) (Potential).
FT	N-linked (GLCNAc. . .) (Potential).
FT	N-linked (GLCNAc. . .) (Potential).
FT	N-linked (GLCNAc. . .) (Potential).
FT	N-linked (GLCNAc. . .) (Potential).
FT	N-linked (GLCNAc. . .) (Potential).
FT	N-linked (GLCNAc. . .) (Potential).
FT	N-linked (GLCNAc. . .) (Potential).
FT	N-linked (GLCNAc. . .) (Potential).
FT	CARBOHYD 434 434 P>H: Dominant negative mutant, blocks
FT	MUTAGEN 680 response to Gram-positive pathogens.

FT	CONFLICT	181	181		y -> H (in Ref. 1)	
SEQ	SEQUENCE	795 AA;	9116 MM;	34d8dd175a26c23	CRC64;	
	Query Match		75.7%;	Score 3144.5;	DB 1;	Length 795;
	Best Local Similarity		73.9%;	Pred. No. 5,4e-188;		
	Matches	588;	Conservative % 97;	Mismatches 110;	Indels 1;	Gaps 1;
OY		1	MTKKKEPIVVSFHHVCMLIIITVGTRIPQSDGNEFAVDKSKRGLIHVRKDLPLTKRVLDMS	60		
Db		1	MSQRKRPVIGSFHFCVLCALIVGSMTEPFSNLEBMVSYNNRLTHVRKDLPPRTKLALS	60		
OY		61	ONVIAELVOVSMSPFLSELTVLRLSHNRIOLDLDSVPKPNODLEYLDLSHNOLOKISCHPI	120		
Db		61	ONSISELMRDPISFLSELRVLRSNRIRSLDFHFVFLENODELYDVSNNRLQNISCCPM	120		
OY		121	VSPFHLLSFPDFPALDICKEFGNLQSOLFGLSAMLKQLDKLLPIAHMLSYLLDLRN	180		
Db		121	ASLRHDDSPDFPVULVCKEFGNLTKLTFLGLSAAFRODLLPVAHHLHSCLLDLV	180		
OY		181	YYIKENETESIQIIMAKTLHVHPITSLEPAIQVNI SVNTLGCTQTQINIKLNDNCQVFIK	240		
Db		181	YHIKGESTESIQTPTVTVLHVFPNPNSLFSSOVMSYNALGHLOLSNI KINDEMCQRLMT	240		
OY		241	FLSLTGTGSTLIANTLNHIETTWKCLVRVQOFLMPKREVEYLYNTYLIIIESIREDDTS	300		
Db		241	FLSELTTGGPTLNTLTOHIEFTWCSVKLQFOWPRPREVELYNTYLITERRIDREEFTYS	300		
OY		301	KTYLKALTIIEHTNQVLFQSOTALTYFSENNIMMLTISTPTFIHMLCPASPFFKLANF	360		
Db		301	ETALKSLMIEHKQVLPFKSEKALYSFAEMNKIMLSISTPTFIHMVCPSPSSFITLNF	360		
OY		361	TQNVFTDISFEKCSSTLYKLETLILQXNGKDLFKVGLMKTDMPSELIDVSWNSLESGRH	420		
Db		361	TQNVFTDSVFGCGSTLKRLOTLLIQRBGLKNFFVALMTXOMSSLFTLDVSLNSINHAY	420		
OY		421	KENCOTVESIVLNLSSNMLTDSYFRCLPPRIKYLDHSNKIKSVPRQVYKLEALOELNY	480		
Db		421	DRTCAWAESILVNLSSNMLTGSVFRCLPKRYKLDLHNNRIMSIPRODVTHLQALOELNY	480		
OY		481	AFNSLTDLPGCGSPSSI.SVLI.IIDHNSVSHPSADPFQSCOMKRSIKAGDNPOCCELRUF	540		
Db		481	ASNSLTDLPGCGAASSLSV.LVIDHNSVSHPSBDFPQSCQINRSITAVANNPQCCELRDF	540		
OY		541	VKNIDQVSEVLEEGMPDSYKCDYPESTRGSPLDKOFHSELSCNTLLIVTIGATMYLAY	600		
Db		541	VKNIGWARAREVBEMPDSTRCDYESSKGTALRDPFHSPLSCDTVLLTVITIGATMYLAY	600		
OY		601	TVTSLSCTIYLDL.PWYLRMVCOMTOTRRARRANI.PLEELQRLNQFAAFISYSEHDSAMVSEL	660		
Db		601	TGARFLCYFLDPMWYRM.COMTQTRRHARHPI.PLEELQRLNQFAAFVSYSEHDSAMVGNEL	660		
OY		661	VPLYEKEDIQICLHERFVFGKSIVENIINCIEKSYSITVLSPNPFQSEMCHELYFAH	720		
Db		661	LPLEXEKDIRCCLHERFVFGKSIVENIINFIEKSYPAIFVLSPHFIQSBMCHELYFAH	720		
OY		721	HNLPHESNNMLIILLEPIPONSI.PNXYCHKL.KALMPORTYLOWPEKESKGL.FMANIRAA	780		
Db		721	HNLPHESNNMLIILLEPILONNIPSRYYHKL.RALMAQRTYLEMPTEKGKGL.FMANIRAS	780		
OY		781	FNMKLTLVTEENNIVKS 796			
Db		781	FIMKLTALVNE.DDYKT 795			
RESULT 8						
Q3UV88_MOUSE						
ID Q3UV88_MOUSE	PRELIMINARY;	PRT;	806 AA.			
AC Q3UV88;						
DT 11-OCT-2005,	integrated into UniProtKB/TremBL.					
DT 11-OCT-2005,	sequence version 1.					
DT 07-FEB-2006,	entry version 5.					
DE Adult male bone cDNA, Riken full-length enriched library,						
clone:1983012OH05 product:coll-1-like receptor 6, full insert sequence.						

GN Name=tlr6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone; PubMed=16141072; DOI=10.1126/science.1112014;
 RX STRAIN=C57BL/6J; PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilmink L.G., Aldins V., Allen J.E., Ambesi-Impombato A., Apweiler R., Aurali R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.-P., Choudhary V., Christofels A., Clutterbuck D.R., Cioe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Hummel L., Iacono M., Ieko K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liu S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Moris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakaurchi H., Ng P., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlandi V., Pang K.C., Payan W.J., Pavese G., Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schombach C., Sekiguchi K., Sempile C.A., Seno S., Sessa L., Sheng Y., Shiba T., Shimada H., Shimada K., Silva D., Sincaltr B., Sperling S., Stupka E., Sugita K., Sultana R., Takanaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.H., Yang K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Matick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida T., Imanura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niimoriya N., Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone; PubMed=16141073; DOI=10.1126/science.1112009;
 RX STRAIN=C57BL/6J; PubMed=16141073; DOI=10.1126/science.1112009;
 RA RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone; PubMed=12466851; DOI=10.1038/nature01266;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaide I., Oasato N., Saito R., Suzuki H., Yamanaka I., Kyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanei A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyszewski-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirazane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa J., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone; PubMed=11217851; DOI=10.1038/35055500;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aizawa K., Iwama A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Iwama A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kanukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Koehli H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Steadil F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barn G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P., Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S., Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone; PubMed=11042159; DOI=10.1101/gr.145100;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone; PubMed=11076861; DOI=10.1101/gr.152600;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashtagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Bone;
 RA Arawaka T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Niimura N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
 RA Muramatsu M., Hayashizaki Y.,
 RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: AK137502; BAE23384.1; -; mRNA.
 DR MGI: MGI:1341296; T1r6.
 DR GO: GO:0016021; C:integral to membrane; RCA.
 DR GO: GO:0016020; C:membrane; RCA.
 DR GO: GO:0004888; F:transmembrane receptor activity; RCA.
 DR InterPro: IPR004075; IL1_rcpt_1.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_C.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR000157; TIR.
 DR Pfam: PF00560; LRR_1; 6.
 DR Pfam: PF01463; LRCT; 1.
 DR Pfam: PF01582; TIR; 1.
 DR PRINTS: PR01537; INTRIKN1RF.
 DR PRINTS: PR00019; LEURICHRPT.
 DR SMART: SM00368; LRR_Typ; 1.
 DR SMART: SM00082; LRCT; 1.
 DR SMART: SM00255; TIR; 1.
 DR PROSITE: PS0104; TIR; 1.
 DR Receptor.
 DR KW RECEPTOR.
 DR SEQUENCE 806 AA, 92394 MW, 6FD0CD4CB8FA5741 CRC64;
 Query Match 75.7%; Score 3144.5; DB 2; Length 806;
 Best Local Similarity 73.9%; Pred. No. 5.5e-188;
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 QY 1 MTKDEPIVKSFFHFCMLIIYVTRIQPSDGNFPAVDKSKGILHVPKPLKTKYLDMS 60
 DB 12 MSQDRKPIVGFPHFCALALIVGSMTPFSNELESNWVDYNNRLTHVPKDLPRTRALSDS 71
 QY 61 QNYIAELQVDSVSELTFLRLSHNRILQDLVYKFNQDDEYLDLSHNOLOKISCHPI 120
 DB 72 QNSISELMPDISFSELRVNLSHNRIRSLDPHFPLFNQDDEYLDVSNRLONSCCM 131
 QY 121 VSFRLHDSFNDPKALPICKERGNLSQNLFLGISAMKLOKDLPLPAHLHLSYILLERN 180
 DB 132 ASLRHLDISFNDPVLPCVCKEFGNLTKLTFGLISAQKFDLLPVAHLHLSYILLDVS 191
 QY 161 YIKENEPESLOILNAKTHLVFHPISLFAIQVNISVNTLGLQTLNKLNDNCQVPIK 240
 DB 192 YHKGEESESLOIPRTYVHLVHFHPISLFSVQVNMVSVALGHLQLSNIKILDNENCQRLMT 251
 QY 241 FLSELTGSGTLNFTLNHIETTKWCLVRYFOFLMPKPEVLYNINVTIIESIREDFTS 300
 DB 252 FLSELTGSGTLNFTLNHIETTKWCLVRYFOFLMPKPEVLYNINVTIIESIREDFTS 311
 QY 301 KTKLALTEHTITNOVFLFSQALYTVFSEKNIIMMLTISDTPFIHMLCPHASTFEKFLNF 360
 DB 312 ETALSKLMIEHVKNOVFLFSQALYTVFSEKNIIMMLTISDTPFIHMLCPHASTFEKFLNF 371
 QY 361 TONVFTDSFEKCTLVKLETLILQKNGKDLFKYGLMKMKPSSLEILDVSNWNSLESQH 420
 DB 372 TONVFTDSFEKCTLVKLETLILQKNGKDLFKYGLMKMKPSSLEILDVSNWNSLESQH 431
 QY 421 KENCTWVESIVLNTSSNMLTDSVFCPLPRIKVLDLHSNKTSKVPQVVKLEALQELNV 480
 DB 432 DRTCAWABEIIYVNTSSNMLTDSVFCPLPRIKVLDLHSNKTSKVPQVVKLEALQELNV 491
 QY 491 AENSITLDPGCGSSLSVLIIDHNSVSHPSADFPQSCQKMSIKAGDNPFQCTCELAEF 540
 DB 492 ASNSITLDPGCGSSLSVLIIDHNSVSHPSADFPQSCQKMSIKAGDNPFQCTCELAEF 551

QY 541 VKNIQVSEVLEGMPDYSKYCDYPSYRGSPLKDFHMSLSGNTLLITIGATMLVLAV 600
 DB 552 VKNIGVAREVEGMPDYSKYCDYPSYRGSPLKDFHMSLSGNTLLITIGATMLVLAV 611
 QY 601 TVTSLCIYLDLPWYLRMVCQWOTRRARNIPLEELORNLQFPAFISYSEHSAWYKSL 660
 DB 612 TCAPLCYVFDLPWYLRMVCQWOTRRARNIPLEELORNLQFPAFISYSEHSAWYKSL 671
 QY 661 VPLEKEDPQILHERNPVPKSIYENIINCEKYSKSFVLSNPNVQSEMHYELFAH 720
 DB 672 LPELKEDPQILHERNPVPKSIYENIINCEKYSKSFVLSNPNVQSEMHYELFAH 731
 QY 721 HNLPHGSSNLLIILLEPIPNISPNKYHKLKALMTQRTYLOMPKESRGLFWANIRAA 780
 DB 732 HNLPHGSSNLLIILLEPIPNISPNKYHKLKALMTQRTYLOMPKESRGLFWANIRAS 791
 QY 781 FNMKLTLYENNDVKS 796
 DB 792 FIMKLTLYENNDVKS 806
 RESULT 9
 ID Q7PC5 MOUSE PRELIMINARY; PRT; 806 AA.
 AC Q7PC5;
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2003, sequence version 1.
 DT 07-FEB-2006, entry version 14.
 DE Toll-like receptor 6.
 GN Name=TLR6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C3H/He; TISSUE=Osteoblast;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton W., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C3H/He; TISSUE=Osteoblast;
 RA Strausberg R.,
 DB Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: BC055366; AAH53366.1; -; mRNA.
 DR HSP: Q15399; 1FV.
 DR SMR: Q7PC5; 641-796.
 DR Ensembl: ENSMUSG0000051498; Mus musculus.

DR MGI:1341296; TIR6.
 DR GO:GO:0016021; C:integral to membrane; RCA.
 DR GO:GO:0016020; C:membrane; RCA.
 DR GO:GO:0004888; F:transmembrane receptor activity; RCA.
 DR InterPro: IPR004075; IIL_rcpf_1.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_C.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR000157; TIR.
 DR Pfam: PF00560; LRR_1; 6.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF01582; TIR; 1.
 DR PRINTS: PR01537; INTRLNK1R1F.
 DR PRINTS: PRO0019; LEURICRPT.
 DR SMART: SM00369; LRR_Typ; 1.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00255; TIR; 1.
 DR PROSITE: PS0104; TIR; 1.
 DR Receptor.
 SQ SEQUENCE 806 AA; 92408 MW; 24830B28EB3C3546 CRC64;

Query Match 75.7%; Score 3143.5; DB 2; Length 806;
 Best Local Similarity 73.7%; Pred. No. 6,4e-188;
 Matches 587; Conservative 98; Mismatches 110; Indels 1; Gaps 1;

1 MTKDEPIVSKFHFVCLMIIIVGTRIQPSDGNFPAVDKSKRGILHVPKDLPLTKVLDMS 60
 12 MSQDKRPVIGSFHFICALALIVGSMTPPNELESVDYNNRULTHVPKDLPRRTALIS 71
 61 QNYIAELOVDMSPFSELVTLRSLSHNRIOQLDLVFKENODLEYLDLSHNOLOKISCHI 120
 72 QNSISELMKPDISFISELRVLRSLSHNRIRSLDFHVEFLFQDLEYLDVSHNRLONSICPM 131
 121 VSRHLDSFNDPKALPTICKERGNISQNLFLGISAMKLOKDLLPRAHLSYIILDLRN 180
 132 ASLRHLDSFNDPDLVPCKEFGNLTKLFLGISAKRFQDLPLPAHLSICLLDLVS 191
 181 YYIKENETESIQIILNAKTLHLVHPPTSLFAIOWNISVNTLGLQLOTNKLNDNCQVFIK 240
 192 YHKGGEFTSDIQIPNTYVHLVHPHPSLFSVOYVNSVNAHGLQLSNITKDNENQORLMT 251
 241 FLSSELRGSLTLNFTLNHIETWKCIVRVFOFLMPKRVYLNINYLTIIESIREDFYTS 300
 252 FLSSELRGPTLNTVLQHIETWKCYSVKLFQFFWPRPVEYLNINYLTERIDREFTYS 311
 301 KTTLKALTTEHTTNOVFLFSQRLATVSENNIMLTISDTPPIHMLCPHASTREKFLNF 360
 312 ETALKSLMIEHVKNQVFLFSKALYVSFAEMNIKMLISDTPFIHWVCPSPSSFTFLNF 371
 361 TONVFTDSIFEKSGTLVKLETTIIONKNGKDLFKVGLMTKDMPSLETLVSNNSLESGRH 420
 372 TONVFTDSVFGGCSITKRLQTLILQNGKLNKFFKALMKNNSSLETLVSNLSNLSHAY 431
 421 KENCTVSEIIVNLSSNMLTDSVPRCLPPIRIKVIDLHNSNKISKVQVYVKEALQELNV 480
 432 DRTCAWABSIIVNLSSNMLTDSVPRCLPPIRIKVIDLHNSNKISKVQVYVKEALQELNV 491
 481 AFNSLTDLFGCGSFSSLSVLIIDHNSVSHPSADFFOSCGQMSIKAGDNPQCTGRLRF 540
 492 ASNSLTDLFGCGAFSSLSVLIIDHNSVSHPSADFFOSCGQMSIKAGDNPQCTGRLRF 551
 541 VNINIOVSEVLGMDPSYKCDYPRSGSPDKDFMSELSCTLLIYTGTMVLAV 600
 552 VNINIGVAREVAVGMDPSYKCDYPRSGSPDKDFMSELSCTLLIYTGTMVLAV 611
 601 TVTSLCIYDLPLMYLWVCOMTQTRRRANIPLEELQORNLOPRAPIYSSEHDSAWKSEL 660
 612 TGAPFLCYLDLPMYVWMLQWOTQTRRAHPIPLEELQORNLOPRAPIYSSEHDSAWKSEL 671
 661 VPLEKEDIQICLHERNVPKGSIVENININCTIKSKYSIFVLSPNFVQSEWCHELYEPH 720
 672 LBNLEKDDIRVCIHERNFVPGKSIENININTEKSKYKALFVLSPHFIOSEWCHELYEPH 731

Qy 721 HNLFEHSGNNIILILEPIONSI PNKYHKLKALMTORTYIQWPKSKGLFWANTRAA 780
 Db 732 HNLFEHSGNNIILILEPIONSI PNKYHKLKALMTORTYIQWPKSKGLFWANTRAA 791
 Qy 781 FNMKLTIVTENNDYKS 796
 Db 792 FIMKLAIVNE-DDVKT 806

RESULT 10
 TLR1 HUMAN
 ID TLR1_HUMAN STANDARD; PRT; 786 AA.
 AC Q15399; Q15452; Q9UG90;
 DT 31-JAN-2002, integrated into UniProtKB/Swiss-Prot.
 DT 31-JAN-2002, sequence version 2.
 DT 07-MAR-2006, entry version 57.
 DE Toll-like receptor 1 precursor (Toll/interleukin-1 receptor-like protein) (TIL) (CD281 antigen).
 GN Name=TLR1; Synonyms=K1AA0012;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Erythrocyte;
 RX MEDLINE=98118556; PubMed=9435236; DOI=10.1073/pnas.95.2.588;
 RA Rock P.L., Hardman G., Timans J.C., Kastlein R.A., Bazan J.F.;
 RT "A family of human receptors structurally related to Drosophila Toll."
 RL Proc. Natl. Acad. Sci. U.S.A. 95:588-593(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Bone marrow;
 RX MEDLINE=96051387; PubMed=7584026; DOI=10.1093/dnares/1.1.27;
 RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y., Sato S., Nagase T., Seki N., Ishikawa K., Tabata S.;
 RT "Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1."
 RT cell line KG-1."
 RL DNA Res. 1:27-35(1994).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Brain;
 RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
 RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glasel S., Ansong W., Boecker M., Bloecher H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N., Mewes H.-W., Oltensweider B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.;
 RT "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs."
 RL Genome Res. 11:422-435(2001).
 RN [4]
 RP PROTEIN SEQUENCE OF 25-39.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally verified cleavage sites."
 RL Protein Sci. 13:2819-2824(2004).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF TIR DOMAIN.
 RX MEDLINE=20531768; PubMed=11081518; DOI=10.1038/35040600;
 RA Xu Y., Tao X., Shen B., Hornig T., Medzhitov R., Manley J.L., Tong L.;
 RT "Structural basis for signal transduction by the Toll/interleukin-1 receptor domains."
 RL Nature 408:111-115(2000).
 CC -!- FUNCTION: Participates in the innate immune response to microbial agents. Cooperates with TLR2 and modulates the response to microbial constituents. Acts via MyD88 and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory

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CC response (By similarity).
CC - SUBUNIT: Binds TLR2 via their respective extracellular domains.
CC Binds MYD88 via their respective TIR domains (By similarity).
CC - SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
CC phagosomes (By similarity).
CC - TISSUE SPECIFICITY: Ubiquitous. Highly expressed in spleen, ovary,
CC peripheral blood leukocytes, thymus and small intestine.
CC - SIMILARITY: Belongs to the Toll-like receptor family.
CC - SIMILARITY: Contains 8 LRR (leucine-rich) repeats.
CC - SIMILARITY: Contains 1 TIR domain.
CC -----
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CC -----
DR EMBL, U98540; AAC34137.1; -; mRNA.
DR EMBL, D13637; BAA02801.2; ALT_INIT; mRNA.
DR EMBL, AL050262; CAB43364.1; -; mRNA.
DR PIR, T08664; T08664.
DR PDB, 1FYV; X-ray; A=625-785.
DR Ensembl, ENSG00000174125; Homo sapiens.
DR H-InvDB, HIT0004160; -.
DR HGNC, HGNC:11847; TLR1.
DR MIM, 601194; gene.
DR GO, GO:0005887; C:integral to plasma membrane; TAS.
DR GO, GO:0045335; C:phagocytic vesicle; ISS.
DR GO, GO:0005886; C:plasma membrane; TAS.
DR GO, GO:0004888; F:transmembrane receptor activity; NAS.
DR GO, GO:0042497; F:triacylated lipoprotein binding; ISS.
DR GO, GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR GO, GO:0042495; P:detection of triacylated bacterial lipoprotein; ISS.
DR GO, GO:0006955; P:immune response; TAS.
DR GO, GO:0042116; P:macrophage activation; NAS.
DR GO, GO:0045410; P:positive regulation of interleukin-6 biosyn. .; ISS.
DR GO, GO:0042535; P:positive regulation of tumor necrosis facto. .; ISS.
DR GO, GO:0007165; P:signal transduction; TAS.
DR InterPro, IPR004075; IL1 rcpt_1.
DR InterPro, IPR001611; LRR.
DR InterPro, IPR000483; LRR C.
DR InterPro, IPR003591; LRR_C.
DR InterPro, IPR000157; TIR.
DR Pfam, PF00560; LRR_1; 7.
DR Pfam, PF01463; LRRCT; 1.
DR Pfam, PF01582; TIR; 1.
DR PRINTS, PR01537; INTRIKN1R1P.
DR PRINTS, PR00019; LEURICHRPT.
DR SMART, SM00082; LRRCT; 1.
DR SMART, SM00255; TIR; 1.
DR PROSITE, PSS0104; TIR; 1.
KW 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immune response; Inflammatory response; Innate immunity;
KW Leucine-rich repeat; Membrane; Polymorphism; Receptor; Signal;
KW Transmembrane.
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FT TOPO_DOM 25 580
FT TRANSMEM 581 601
FT TOPO_DOM 602 786
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FT REPEAT 19509 19533
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FT REPEAT 19561 19585
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Db 365 FENCGHLELETLILQNMQLKELSKIAEMTQMKSLOQDIDSONSVSYDEKGDGCSWTKS 424
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Db 425 LLSLNMSSNLTLDITFRCLPPIKYLIDHSNKIKSVKQVYVLEALQELNVAFNLSITLDP 484
Qy 490 GCGSFSSLSVLLIDHNSVSHPSADPFQSCQKRSIKAGDNPQCTCELRFPYKNIIDQVSS 549
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Qy 550 EYLBGMPDSYKCDYESTRGSPLKDFHMSLSNLTLLIVTIGATMLVLAIVTSLCTYL 609
Db 545 EYLBGMPDSYKCDYESTRGSPLKDFHMSLSNLTLLIVTIGATMLVLAIVTSLCTYL 604
Qy 610 DLPWLRVACWQOTQRRRARNIPLEELQRLNLFPHAFISYSEHDSAMVSELPVYLEKEDI 669
Db 605 DLPWLRVACWQOTQRRRARNIPLEELQRLNLFPHAFISYSEHDSAMVSELPVYLEKEDI 664
Qy 670 QICLHERNFVPEKSIIVENINICIEKSYKSI FVLSNPFVQSEWCHELYFAHNLPHBSGN 729
Db 665 QICLHERNFVPEKSIIVENINICIEKSYKSI FVLSNPFVQSEWCHELYFAHNLPHBSGN 724
Qy 730 NILILLEPIPNQSIIPNKYHKALKALMTQRTYIQMPKESKRGLPFANIRAAFNMKLT 786
Db 725 STILILLEPIPNQSIIPNKYHKALKALMTQRTYIQMPKESKRGLPFANIRAAFNMKLT 781
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AC Q32MK3;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Toll-like receptor 1.
GN Name=TLR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OK NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388557; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheaffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda N.T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultig S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bladesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RN NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC
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DR EMBL, BC109094; AA109095.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
KW Receptor.
SQ SEQUENCE 786 AA; 90290 MW; 1406C6FB5847F58 CRC64;

Query Match 68.1%; Score 2830; DB 2; Length 786;
Best Local Similarity 69.5%; Pred. No. 2,5e-168;
Matches 540; Conservative 92; Mismatches 143; Indels 2; Gaps 1;

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Qy 132 DFKALPICKERGNLSQNLFLGLSAMKQKDLPLPAHLHSYLLDLNRYIKENETESL 191
Db 125 AFDALPICKERGNMSQLKFLGLSTHLEKSVLPFAHLNISKVLVLGETYGEKEDPGL 184
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Db 245 KLSLTLNNIETWMSFRIQLQVHTTWTFYSISNVKQGLDPRDDYSGTSLKALSI 304
Qy 310 EHTNQVLFQSALYTVFSENNIMLTISDTPFIHMLCPHAPSFEKELNFTQVFTDSI 369
Db 305 HQVYSDVGFPGQSYIYELFNMNINIKFTVSGRBMVHMLCPKSIISFELHLDSPNNLLTFTV 364
Qy 370 FEKSGTLVYKLTLLIQKNGKDLFVYGMTKDMPSLEILIDYSWNSLBEGRHKENCTWES 429
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Qy 430 IVNLNLSNMILTDSPFRCLPPIKYLIDHSNKIKSVKQVYVLEALQELNVAFNLSITLDP 489
Db 425 LLSLNMSSNLTLDITFRCLPPIKYLIDHSNKIKSVKQVYVLEALQELNVAFNLSITLDP 484
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Db 485 GCGSFSSLSVLLIDHNSVSHPSADPFQSCQKRSIKAGDNPQCTCELRFPYKNIIDQVSS 544
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Db 545 EYLBGMPDSYKCDYESTRGSPLKDFHMSLSNLTLLIVTIGATMLVLAIVTSLCTYL 604
Qy 610 DLPWLRVACWQOTQRRRARNIPLEELQRLNLFPHAFISYSEHDSAMVSELPVYLEKEDI 669
Db 605 DLPWLRVACWQOTQRRRARNIPLEELQRLNLFPHAFISYSEHDSAMVSELPVYLEKEDI 664
Qy 670 QICLHERNFVPEKSIIVENINICIEKSYKSI FVLSNPFVQSEWCHELYFAHNLPHBSGN 729
Db 665 QICLHERNFVPEKSIIVENINICIEKSYKSI FVLSNPFVQSEWCHELYFAHNLPHBSGN 724
Qy 730 NILILLEPIPNQSIIPNKYHKALKALMTQRTYIQMPKESKRGLPFANIRAAFNMKLT 786
Db 725 STILILLEPIPNQSIIPNKYHKALKALMTQRTYIQMPKESKRGLPFANIRAAFNMKLT 781
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AC Q32MK4;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Toll-like receptor 1.
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GN Name=TLRL;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 NCBI_TaxID=9606;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RG NIH MGC Project;
 RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
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 DR EMBL: BC109093; AAI09094.1; -; mRNA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
 KW Receptor.
 SQ SEQUENCE 786 AA; 90291 MW; 1BPCCE5E42EA542 CR664;
 Query Match 68.1%; Score 2829; DB 2; Length 786;
 Best Local Similarity 69.5%; Pred. No. 2,9e-168;
 Matches 540; Conservative 91; Mismatches 144; Indels 2; Gaps 1;
 QY 12 FHFVCLMIITVGTTRIOFSDGNFAYDKSRGGLIHPKDLPLTKTVLMDSQNTIAELQVSD 71
 DB 5 FHFALIFMLLIQIRIQLSSESEFLVDRSNGLIHPKDLISQTKTILINISQNTISELWTSDD 64
 QY 72 MSFISELTVLRSHNRIOQLDLVSFKFNODLEVLDLDSHNOLOKISCHPIVSRHLDLSPN 131
 DB 65 ILSLSKRLILISHNRIOQLDLVSFKFNODLEVLDSHNLKYLKISCHPIVSRHLDLSPN 124
 QY 132 DFKALPICKFEGNLSQNLNGLSANKLOQLDLPIAHLHLYTLDLRNYITKENETESL 191
 DB 125 AFDALPICKFEGNMSQNLKFLGLSTHLEKRSVLPFAHLNISKVLVGLGTGEKEDPEGL 184
 QY 192 QILNAKTLHVPHPISLPAIQNVISVNTLGCQLTNIK-LVDDNCQVATIKLSELTRGS 249
 DB 185 QDFNESHIVPPTNKEFPIIDVASKIVANLELSIKVLBDNKSYSYLSLAKQTNP 244
 QY 250 TLNLTNLNIIETTWKCLVRFQFLWPKPVEYINIVNLTIIIESIREEDFTYSKTLTKALTI 309
 DB 245 KLSNLTNNIETTWMSPIRIQLVHTTWYPSISVVKLQGLDPRDPYSGSLKALSI 304
 QY 310 EHTIQTQVFLFSQTLATYVSENNIMMLTISDTPFIHMLCPHAPSTFKFLNFTQNVFTDSI 369
 DB 305 HQVADVDFGFPQSYIETIFSNMNIKNQFTVSGTRVMHMLCPSTKISPLHLDFSNMLITDTIV 364

QY 370 FEKCSITVLKLETLILQKNGKJDKLFVKGLMTKMPSLIEDVSMNSLDSGRHKENCTWVES 429
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 DB 605 DLPWYLRVQWQTRRRARNIPLEELQNLQFPAFISYSEHSDSAVSKELVYLEKEDI 664
 QY 670 QICLHERNPVKSIYENITNICEKSYKSI FVLSRPFQSEKCHYELFAHNLFPREGSN 729
 DB 665 QICLHERNPVKSIYENITNICEKSYKSI FVLSRPFQSEKCHYELFAHNLFPREGSN 724
 QY 730 NLILILPEIPONSIPNKYHKLKALMTORTYLOMPKESKRGFLFMANIPAFNMKLT 786
 DB 725 SLILILPEIPONSIPNKYHKLKALMTORTYLOMPKESKRGFLFMANIPAFNMKLT 781
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 ID 05FMG5 HUMAN PRELIMINARY; PRT; 786 AA.
 AC 05FMG5;
 DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2005, sequence version 1.
 DE 07-FEB-2006, entry version 8.
 DE Toll-like receptor 1.
 GN Name=TLRL;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 NCBI_TaxID=9606;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;
 RG NIH MGC Project;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

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 DR EMBL: BC089403; AA89403.1; -; mRNA.
 DR SMR: OSFMC5; 625-785
 DR Ensembl: ENSG00000174125; Homo sapiens.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR004075; IL1 rcpt 1.
 DR InterPro; IPR003016; LipoyL_BS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_C.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR00157; TIR.
 DR Pfam; PF00560; LRR_1; 7.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PRO1537; INTRLNK1RLF.
 DR PRINTS; PRO0019; LEURICHRPT.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS00189; LIPOYL; UNKNOWN_1.
 DR PROSITE; PS50104; TIR; 1.
 DR KX
 DR RECEPTOR.
 SQ SEQUENCE 786 AA; 90267 MW; 6B9B673F6E47BF3A CRC64;
 Query Match 68.1%; Score 2828; DB 2; Length 786;
 Best Local Similarity 69.5%; Pred. No. 3.3e-168;
 Matches 540; Conservative 92; Mismatches 143; Indels 2; Gaps 1;
 QY 12 FHFVCLMIITVGRIOFSDGNEFPAVDKSRGLIHVPKDIPLTKVLDMSONYIAELQVSD 71
 DB 5 FHFALIFMLIDQIRIQLSSESEFLVDRSKGDIHVPKDSQKTTILNISQNIYSELMTSD 64
 QY 72 MSFSELTVRLSHNRIOQLDLSVPEKNOLELYLDLSHNOLOKISCHPIVSRHILDSN 131
 DB 65 ILSLKLRLIISHNRIOQLDLSVPEKNOLELYLDLSHNRIOKISCHPIVSRHILDSN 124
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 DB 125 AFDAIPICKERFGNMQKFLGISTHLEKSSVLPFAHINISKVLVLGRTYGEKEDPGEL 184
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 QY 310 EHIITQVFLFSOTALYTVFSENNIMMLISDTPFIHMLCPHAPSTFEKFLNFTQNVFTDSI 369
 DB 305 HQVAVDVGFPGQSYIYEIIFSNMNIKNFTVSGTRMVMMLPSKISPLINLDFSNLLTDIV 364
 QY 370 FEKCGTLYKLETLIIQKNGLKDLFKVGLMTKMPSELIELIDVSNISIESGRHKENCTWBS 429
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 DB 605 DLPLWLRVCOMTQTRRRARANIPLBELQNLQFHAISYSEHSDSAVNSKELVYLEKEHI 664

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 DB 665 QICLHERNFVPEKSIENINICIEKSYKSIPLVSNFVQSEWCHYEYFAHNLFEHGSN 724
 QY 730 NILILLEPIRONGIPNKYHKLKALMTORTYLOWPEKSKGFLFANIRAAFNMLLT 786
 DB 725 SLILLEPIRONGIPNKYHKLKALMTORTYLOWPEKSKGFLFANIRAAFNMLLT 781
 RESULT 14
 Q6FI64_HUMAN PRELIMINARY; PRT; 786 AA.
 AC Q6FI64;
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE TLRI protein.
 GN Name=TLRI;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo
 OC NCBI_Taxid=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: CR533562; CAC38593.1; -; mRNA.
 DR SMR: OSF164; 625-785.
 DR Ensembl: ENSG00000174125; Homo sapiens.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR004075; IL1 rcpt 1.
 DR InterPro; IPR003016; LipoyL_BS.
 DR InterPro; IPR000483; LRR_C.
 DR InterPro; IPR00157; TIR.
 DR InterPro; IPR00157; LRR_Typ.
 DR Pfam; PF00560; LRR_1; 7.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PRO1537; INTRLNK1RLF.
 DR PRINTS; PRO0019; LEURICHRPT.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS00189; LIPOYL; UNKNOWN_1.
 DR PROSITE; PS50104; TIR; 1.
 DR KX
 DR RECEPTOR.
 SQ SEQUENCE 786 AA; 90163 MW; DB6B54E684009284 CRC64;
 Query Match 67.8%; Score 2817; DB 2; Length 786;
 Best Local Similarity 69.2%; Pred. No. 1.6e-167;
 Matches 538; Conservative 92; Mismatches 145; Indels 2; Gaps 1;
 QY 12 FHFVCLMIITVGRIOFSDGNEFPAVDKSRGLIHVPKDIPLTKVLDMSONYIAELQVSD 71
 DB 5 FHFALIFMLIDQIRIQLSSESEFLVDRSKGDIHVPKDSQKTTILNISQNIYSELMTSD 64
 QY 72 MSFSELTVRLSHNRIOQLDLSVPEKNOLELYLDLSHNOLOKISCHPIVSRHILDSN 131
 DB 65 ILSLKLRLIISHNRIOQLDLSVPEKNOLELYLDLSHNRIOKISCHPIVSRHILDSN 124
 QY 132 DFKALPICKERGNLSQNLFLGLSANKLOQLDLPLIAHLSTYLLDLRNYIKENETSL 191
 DB 125 AFDAIPICKERFGNMQKFLGISTHLEKSSVLPFAHINISKVLVLGRTYGEKEDPGEL 184
 QY 192 QILNKTALHVPHTSLFAIQVNISVNTLGCQLTNIK--LNDNQCQVFIKFLSELTRGS 249
 DB 185 QDFNTESLHIVPTKKEFHFIIDVSKVTANLESLNICKVLBDNKSQYFLSLAKLQTNP 244

```

OY 250 TLINLTINIIETTWKCLVAVFOGLMPKPEYINVLNLTIES:REEDFTYKSTLTALTI
OY 245 KLSLTIINNIETTWNSFIILQLVHTTYWYSSISNVKLOGLDFRDFYSGISLRALSI
Db 310 EHIITNOVFLFSQATLYVTFSENNIMMLITSDPFIHMLCEHASTKFLNFTONVFTDSI
OY 305 HQVSDVDFGPOSYIVIEIFSNMNIKNFVTVSGTRMVMHLCPSKISPIFLHDPSNNLLTDIV
Db 370 PEKCSITVLELTLIIQXNGLKDLFKGLMTKOMPSEILDVSNNSLSGCHKENCYVES
OY 365 FENCGHLELELTLIIQMNOLKELSKIAEMTTQWKSJQOLDIISONSVSYDEKKDCGWTKS
OY 430 IYVLNLSNMLTDSVRCPPRIKIVYDDLNSNKIKSPKQOVYKLEALQELNVAFNSLTDLP
OY 425 LLSLWMSNMLTDTIFRCPLCPRIKIVYDDLNSNKIKSPKQOVYKLEALQELNVAFNSLTDLP
OY 490 GCGSFSSLSVLLIIDHNSVSHPSADFPQSCQKMSIKAGDNPFQCTCELRBFVNKDQVS
Db 485 GCGSFSSLSVLLIIDHNSVSHPSADFPQSCQKMSIKAGDNPFQCTCELRBFVNKDQVS
OY 550 EYLEGMPPDSYKCDYPSYRGSPLKDPHMBELSNITLLIYTGATMLVLAVTYTSICYL
OY 545 EYLEGMPPDSYKCDYPSYRGSPLKDPHMBELSNITLLIYTGATMLVLAVTYTSICYL
OY 610 DLPWTLRWCOMTQTRRRARANIPLBELQNLQPHAFISYSEHDSAWKSELVYLPKEDI
Db 605 DLPWTLRWCOMTQTRRRARANIPLBELQNLQPHAFISYSEHDSAWKSELVYLPKEDI
OY 670 QICHERNFVPEKSIYENIITCIEKSYKSIYVLSPNFVQSEWCHYELFYAHNHLFHEGSN
Db 665 QICHERNFVPEKSIYENIITCIEKSYKSIYVLSPNFVQSEWCHYELFYAHNHLFHEGSN
OY 730 NLILILBIPONSIIPNKTHKIKALMTQTYILOMPREKSKGGLFANINIRAFPMKLT
Db 725 SLILILBIPONSIIPNKTHKIKALMTQTYILOMPREKSKGGLFANINIRAFPMKLT
Cc RESULT 15
Cc QALDR7_PIG PRELIMINARY, PRT, 796 AA.
Cc ID QALDR7_PIG
Cc AC QALDR7;
Cc DC 02-AUG-2005, integrated into UniProtKB/TrEMBL.
Cc DT 02-AUG-2005, sequence version 1.
Cc DT 07-FEB-2006, entry version 3.
Cc DE Toll-like receptor 1.
Cc GN Name=TLR1;
Cc OS Sus scrofa (Pig) .
Cc OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cc OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;
Cc OC Sus.
Cc OX NCBI_Taxid=9823;
Cc RX N1
Cc RN NUCLEOTIDE SEQUENCE.
Cc RC TISSUE=Small intestine;
Cc RA Shinkai H., Muneta Y., Suzuki K., Eguchi-Ogawa T., Awata T.,
Cc RA Uenishi H.;
Cc RT "Complete nucleotide sequence in the porcine genomic region containing
Cc RT Toll-like receptors 1, 6, and 10 genes and their expression
Cc RT analysis.";
Cc RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
Cc CC
Cc CC -----
Cc CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Cc CC Distributed under the Creative Commons Attribution-NoDerivs license
Cc CC -----
Cc DR EMBL, AB219564; BAB06146.1; -, mRNA.
Cc DR SMK; QALDR7, 629-789.
Cc DR GO; GO:0016020; C:membrane; IEA.
Cc DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
Cc DR InterPro; IPR004075; IL1 rcpt_1.
Cc DR InterPro; IPR001611; LRR.
Cc DR InterPro; IPR000483; LRR_C.
Cc DR InterPro; IPR003591; LRR_Typ.

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DR InterPro; IPRO00157; TIR.
DR Pfam; PF00560; LRR_1; 7.
DR Pfam; PF01582; TIR_1.
DR PRINTS; PRO1537; INTRICKN1R1F.
DR PRINTS; PRO0019; LEURICHRPT.
DR SMART; SMO0082; LRCT; 1.
DR SMART; SMO0255; TIR; 1.
DR PROSITE; PSS0104; TIR; 1.
KW Receptor.
SQ SEQUENCE 796 AA; 90967 MW; 396C3D69B99442C4 CEC64;

Query Match	63.9%	Score 2654.5;	DB 2;	Length 796;
Best Local Similarity	63.5%	Pred. NO. 2.4e-157;		
Matches 500; Conservative	124;	Mismatches 158;	Indels 5;	Gaps 2;

Qy	1	MTKQKBPVYSHFHVCCMIIIYVGRIOFOSDNEFAVYDKSRKGLIHPKDIPLTKIVLDS	60
Db	1	MTKENLSTI---FHHAIIFILLETRIQJSESEVYLVDSKSTGLIHPKDIJSELETTILDS	57
Qy	61	QNYIAELQVSDMSFSELTIVLRLSHNRIOJLDLDSVFENQDLEYLDJSHNOLOKISCHPI	120
Db	58	QNSISELQSDJSDLSKLRVPIISHNRIQYLDVSVFENQDELEYLDJSHNLEKISCHPM	117
Qy	121	VSPFHDLSTRNDFPALPICKEFGNLSQLNLYGLSAMKLOKJLDLPIAHLSSTYLLDLRN	180
Db	118	LNELGHLDSFPAFPALPICOFEGSMFOLEFGLSATOLOKSSVPIAHLEHIGKVLVLGD	177
Qy	181	YYIKENETSELOLNATKTLVHFHPTSLPAPQVNI SVNTLGCLOLTINIK--LNDNQCVF	238
Db	178	SYGRBEPBESIQDINTOSTLHI VPPKGFHFHMLDVSVTA VNLNLSNRICVLDNGCHF	237
Qy	239	IKFSELSTRGSTLNFPLNHIETWKCLVBFQFLMPKPEVYALINVLITIEISREEDFT	298
Db	238	QNVYLKLOKMSKLSNLFLNNIETMWSFIITLOQVWRTSIEFYSISVYKQGOJDLPRFD	297
Qy	299	YSKTTLKALITTEHTNOVFLFSQCALYTVSSENNIMMLTISDPFIHMLCPHAPSTREKL	358
Db	298	YSDTSLKALSLHQVSEVFPFQSYIYKIFSNMNIQYLVATSMVHMVWCPSQISPELYL	357
Qy	359	NFTQNVYTDTSIFEKCSFLVYKLETLILQKNGKJDLFKYGLMTKDMPSLEILDVSNNSLESG	418
Db	358	DFSNALLTDWFKKCAVLNANTLSLOMNOKELVNIYHMTKEHOSLOQJLDVSOJTLRYD	417
Qy	419	RHKENCTWSEIVVLNLSNMJLTDVSRCLPPIKIVLDLHSNKITKSVKQVYVKEALQOEL	478
Db	418	ENEGSCWTGSLSLNLSNLTDSVPRCLPPIKIVLDLHNHRIIRSIPIKDVAHLEALQEL	477
Qy	479	NVAFNLSITDLPGCCSFBSLSVLLIIDHNSVSHPSADFQSCOKMASIYAGDNPFQCTEELR	538
Db	478	NVASNSLPAHLPGCCSFBSLSILIIDVNSINPSPADFQSCQIKRSLAKGNPFQCTEELR	537
Qy	539	EPVKNIDQVSEVYLEGMPDSYKCDYPRSYSGSPKDKPHMSELSGNTITLYITIGATMVLV	598
Db	538	DFIOSLQGVSSDVVESMPDSIECEYPPSYKGTLLKDRVSELSGNTALLIYITIGTAL	597
Qy	599	AVTVTSLCTIYLDLPWYLRMVCOMTOTERRARANIPLBELQBNLOPHAFISYSEHDSAWKS	658
Db	598	ALMPTGLCYVFDLPWYLRLMCOMTOTERRARANVPLELOQTLQPHAFISYSGHDSAWKN	657
Qy	659	EIVPYLEKEBIOICLHHRNFVPGKSIVENITNCLEKSYKSI FVLSBNFVQSEWCHYELXF	718
Db	658	ELLBNVEKEBKIICLHHRNFVPGKSIMENITNCIEKSYKSI FVLSBNFVQSEWCHYELXF	717
Qy	719	AHHNLPFHGSGNNILILLEBPIQNSIPENKXHKLKALMTQRTYLOMPKEKSRGLGFMANIR	778
Db	718	AHHNLPFHGSGDNILILILDISIPQYSIPSSYHKULKALMAQRTYLEWPREKSGHGLGFMANLR	777
Qy	779	AAPNMKL 785	
Db	778	ASINIKL 784	

Job time : 162 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 2, 2006, 22:53:30 ; Search time 22 Seconds

(without alignments)
3461.297 Million cell updates/sec

Title: US-10-732-796A-12

Perfect score: 4154

Sequence: 1 MTGXKEPIVKSHPFVCLMII.....IPAAFNKMLTLVTENNVDYKS 796

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2820	67.9	786	2	T08664 Toll protein-like
2	406.5	9.8	1097	2	A29943 Toll protein precu
3	285.5	6.9	1066	2	T15864 hypothetical prote
4	274	6.6	1385	2	T13887 c1r protein - fru1
5	268.5	6.5	1039	2	T22117 hypothetical prote
6	268.5	6.5	1389	2	T13852 gene wheeler prote
7	244.5	5.9	987	2	T50850 receptor protein K
8	238	5.7	662	2	S42799 gaip precursor - h
9	235	5.7	1531	2	T42218 slit-1 protein hom
10	233	5.6	1469	2	B3665 slit protein 2 pre
11	233	5.6	1480	2	A3665 slit protein 1 pre
12	230.5	5.5	921	2	B86234 hypothetical prote
13	226.5	5.5	559	2	T42998 Ras-binding protei
14	225.5	5.4	1025	1	A57676 protein kinase Xa2
15	225	5.4	855	2	T07015 Cf-4A protein - to
16	223	5.4	1091	2	A58532 glial cell membran
17	221	5.3	1143	2	T10636 hypothetical prote
18	221	5.3	1692	2	A33988 adenylylate cyclase
19	219	5.3	560	2	A60164 platelet membrane
20	217	5.2	907	2	UG0193 G protein-coupled
21	216	5.2	572	2	T30947 hypothetical prote
22	214.5	5.2	1134	2	T04587 hypothetical prote
23	212	5.1	853	2	T17461 disease resistance
24	211	5.1	661	2	T56258 RPI05 - mouse
25	210	5.1	890	2	B84846 probable receptor-
26	210	5.1	2026	1	OYBY adenylylate cyclase
27	208.5	5.0	983	2	G84524 probable disease r
28	207	5.0	800	2	H84740 hypothetical prote
29	207	5.0	1839	1	OYBYK adenylylate cyclase

30	206	5.0	855	2	T17460 disease resistance
31	205	4.9	1013	2	T10659 probable serine/th
32	205	4.9	1778	2	AF1116 intermin protein
33	204.5	4.9	1523	2	T13953 MEGF5 protein - ra
34	204	4.9	613	2	A88684 protein ACT.2 (imp
35	204	4.9	679	2	T20713 hypothetical prote
36	204	4.9	907	2	JE0176 orphan G protein-c
37	203.5	4.9	845	2	T07039 Hcr9-0 protein - t
38	203	4.9	707	2	T28418 ORF MSY257 leucine
39	202.5	4.9	611	2	T28171 hypothetical prote
40	202	4.9	1166	2	F96598 protein F20N2.4 [l
41	200	4.8	1232	2	T05322 hypothetical prote
42	198.5	4.8	910	2	G84648 probable disease r
43	196	4.7	980	2	H84632 probable receptor-
44	195	4.7	910	2	B96770 hypothetical prote
45	195	4.7	1134	1	A29944 chaoptin precursor

ALIGNMENTS

RESULT 1

T08664

Toll protein-like receptor DKFP54710610.1 - human

QY	12	PHFVCLMIIIVTGRIOFSDNGNEFAVDKSRGHLHYPKDLPKTKVLDMSQNTYAEQVSD 71
DB	5	FFHAIIFMILIRIQLSSESEFLVDRSKGHLHPKDSQKTTINISQNTYSELMTSD 64
QY	72	MSFLSELTVLRLSNRIQLDLVFRFNODELYDLSSHQLOKISCHPIVSFRHLDSFN 131
DB	65	ILSLSKRLILISHNRIQYLDISVFRNQELEYDLSSHVKLSCHPIVNLKHLDSFN 124
QY	132	DKRALPICKERGNLSQANLGLSANKLOKLDLPIAHLSTYLLDRLRYIYKENTESTL 191
DB	125	AFDALPICKERGNLSQANLGLSANKLOKLDLPIAHLSTYLLDRLRYIYKENTESTL 184
QY	192	QLNKAQLHLVHPSTLPAIOVNISVNTLGCQLNFK-LNDNDQCVRIKFSLETTRGS 249
DB	185	QFNTESSHLVPTPTKEFFILDVSVKYANIELSNIKVLEDSKSYLSLAKIQNP 244
QY	250	TLNFTLNHIEETWKCLVRFQFLMPKPYELINYNLTIESIREEDFTYSKTLKALT 309
DB	245	KLSLLTNIEETWKCLVRFQFLMPKPYELINYNLTIESIREEDFTYSKTLKALT 304
QY	310	EHTNOVFPSTALYTVSENNIMLTISDPFIHMLCPHAPSTFKLNFQNVTTDSI 369
DB	305	HQVNSVDFEPQSYIYEIFSNMINKFTVSGTRVMMLCPKISPELHLDNFNNLTDTV 364
QY	370	FKKSGTLVLEFLLLOKNGLDKDFKGLMTKMPSEILDVSNLSGRHKEKNTWES 429
DB	365	FENGCHLLEFLLLOKNGLDKDFKGLMTKMPSEILDVSNLSGRHKEKNTWES 424
QY	430	IVVLNLSNMULDVSFRCLPPIKYLDLHSNKIKSVKQVVKLEALQELNVAFNSITDIP 489
DB	425	LISLNMSSNILDITFRCLPPIKYLDLHSNKIKSVKQVVKLEALQELNVAFNSITDIP 484

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QY 490 GCGSSSSSVLLIIDHNSVSPADPFQSCQKRSIKAGDNPQCTCELEFPYKNIIDOVSS 549
DB 485 GCGSSSSSVLLIIDHNSVSPADPFQSCQKRSIKAGDNPQCTCELEFPYKNIIDOVSS 544
QY 550 EYLBEMPSYKCDYFESYSGSPKDPHMSLSNLTLLVITGATMLVLAIVTSLCITL 609
DB 545 EYLBEMPSYKCDYFESYSGSPKDPHMSLSNLTLLVITGATMLVLAIVTSLCITL 604
QY 610 DLPWYLRWVCOMQOTRRRRARNIPLEELQNLQPHAFISYSEHDSAMVKESELYLEKEDI 669
DB 605 DLPWYLRWVCOMQOTRRRRARNIPLEELQNLQPHAFISYSEHDSAMVKESELYLEKEDI 664
QY 670 QICLHERNFVPGKSIYENIINCIEKSYKSIYVLSPNFVQSEWCHYELYPAHNLPFHESGN 729
DB 665 QICLHERNFVPGKSIYENIINCIEKSYKSIYVLSPNFVQSEWCHYELYPAHNLPFHESGN 724
QY 730 NILILILEPIPNQSIYKPKYHKIKALMTORTYIQMPREKSKRGIFMANITAAEMKLT 786
DB 725 SILILILEPIPNQSIYKPKYHKIKALMTORTYIQMPREKSKRGIFMANITAAEMKLT 781

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RESULT 2

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A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C1Species: Drosophila melanogaster
C1Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C1Accession: A29943
R1Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A1Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, as
A1Reference number: A29943; MUID:88135760; PMID:2449285
A1Accession: A29943
A1Molecule type: DNA
A1Residues: 1-1097 <HAS>
A1Cross-references: UNIPROT:P08953; UNIPARC:UPI0000124883; GB:M19969; GB:J02682; NID:915
C1Genetics:
A1Gene: FlyBase:Fl
A1Cross-references: FlyBase:FBgn0003717
C1Keywords: transmembrane protein
F1-17/Domain: signal sequence #status predicted <SIG>
F18-1097/Product: Toll protein #status predicted <MAT>

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Query Match 9.8%; Score 406.5; DB 2; Length 1097;
Best Local Similarity 22.5%; Pred. No. 1.5e-18;
Matches 203; Conservative 145; Mismatches 321; Indels 235; Gaps 38;

QY 41 RGLIHPKD-----LPKTKVLDNSQNTYIAELQVSDMSFLSELTVLRSLNRIQL 90
DB 160 RRLTPIPNALLTDMENLSHLELRANIEEMPSHLFDLE-----NLESIFGSKLRQ 211
QY 91 LDLSYFKFNQDLEYLDLSHNOLOKISCH-----PIVSFPHL--- 126
DB 212 MERGIFGKMPKQLKQNLMSNQLNHLTKHDPGATSVYLGIDHDNGICBQLPHDVFALHTNV 271
QY 127 ---DLSFNDFKALP-----ICKEFGNLSQLNPLGLSAMKL 158
DB 272 TDINISANLFRSLPGQLFDHNGHNEVRLMNNRVPPLATPSLPLANNQPELQLRLRA-EL 330
QY 159 QKL---DL-----PIAHLSYLLDLRNTYIKENRFE---SLQTLNAKTIHLVHPISLFA 210
DB 331 QSLPDLFEHSTQITNISLGDNLTKTLPTLLEHQVNLISLPLSNRLTHL---PDSLFA 387
QY 211 IQVNI-----SVNTIGCLQITWIKLNDNCOVFIKFLSELFRGSTL 251
DB 388 HTTNLTDLRLBNLLTGISGDIFFSNIGNLVTLVMSKNRLRTIDSRAFVS---TWGLRH 442
QY 252 LNTFNLHLETTWKCLVRFQFLMPKRVEX-----LNIYNLTI--- 295
DB 443 LHLHDNDIDLQOPLDIDIMQTOINSPFGYMGHGLTLNLRNNSIIFVYNDWKATMLQLRL 502
QY 296 DFTYSKTIKALTIEHTITNQVFLFSQATALYVFS-----ENKIMML 336
DB 296 DFTYSKTIKALTIEHTITNQVFLFSQATALYVFS-----ENKIMML 336

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DB 503 DLSTN-NISSIGYDLD---FLSQNLHVNMTNKRRLRALPEDVHLGSGYNNNLVHV 556
QY 337 TISDTPFIMLCPHAPSTFKFLNFTQNV-----FTDSIFEKSGTVYKLETLILQKNGLDL 392
DB 557 DLNDNP---LYVD---CTILWFIQLVGVHKKQYSQFRLDRIVLCQSPNVNLEGPVQI 611
QY 393 FVVGIMTYDMPSLLEILDVSNLSGSRHKE-----NC---TWVESIVVLNLSNMLTSSV 444
DB 612 EPQTLICP-----LDPS-----DDPRERKCPRGNCCHVRTDKALVINCHSGNLTIVPR 660
QY 445 PRCLPERRIKVLDLH--SNKIKSVPK-qVYKLEALQELVAFNSLNDLGCSSFSLSVLI 501
DB 661 LPNLHKMQLMELHNNNTLRLPSANTPGYBSVSLHLAGNNLTSTIVDQLPTVLTILD 720
QY 502 IDHNSVSPSA---DFQSCQKRSIKAGDNPQCTCELEFEV---KNIDQVSSEVLEG 554
DB 721 ISMNILQMLNATVGLFRLRTMKRVRVKLSGNPMWDCCTAKPLLLFTQNPFEI-----G 774
QY 555 WPDYKCDYPESYSGSPKDPHMSLSGN-----ITLLVITGATMLVLAIVT--- 602
DB 775 DENEMVCVNAE---MPTR---MVSLSTNDICPAKGVFIALAVIALTGLAGFTALY 827
QY 603 ---TSLCITYLDLPWYLRWVCOMQOTRRRRARNIPLEELQNLQPHAFISYSEHDSAMVKS 658
DB 828 YKQTEIKIWL---YAHNLWVTE-----EDLDKQKFPDFTSYSHKQDFTLED 875
QY 659 ELVPLYE--KEDIQICLHERNFVPGKSIYENIINCIEKSYKSIYVLSPNFVQSEWCHYEL 716
DB 876 YIVPQLEHGPQKFOUCYHERDMVCGHLPENIMRSVADSRRITVILSQNFIKSEARLEF 935
QY 717 YFAHNLPFHESGNLILILEPIPNQSIYKPKYHKIKALMTORTYIQMPREKSKRGIFMAN 776
DB 936 RAHRSALNEGSRRIIIVYSDI-GDVEKLDLEIKAVLKNMTYLDKWDP-----WFWDK 988
QY 777 IRRA 780
DB 989 LRFA 992

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RESULT 3

```

T15864
hypothetical protein C56E6.6 - Caenorhabditis elegans
C1Species: Caenorhabditis elegans
C1Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C1Accession: T15864
R1Fulton, L.
submitted to the EMBL Data Library, November 1995
A1Description: The sequence of C. elegans cosmid C56E6.
A1Reference number: S69019
A1Accession: T15864
A1Status: preliminary; translated from GB/EMBL/DBJ
A1Molecule type: DNA
A1Residues: 1-1066 <FULL>
A1Cross-references: UNIPROT:Q18902; UNIPARC:UPI00000811D7; EMBL:U39996; NID:g1055114; PT
C1Genetics:
A1Gene: C56E6.6
A1introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 833/3; 892/3; 9

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Query Match 6.9%; Score 285.5; DB 2; Length 1066;
Best Local Similarity 21.0%; Pred. No. 1.1e-10;
Matches 140; Conservative 123; Mismatches 220; Indels 185; Gaps 30;

QY 21 IVGTRIQFSDGNEFAVDKSKRGLIHVPKDLPLKTVLDMSONYIAELQVSDMSFLSELTV 80
DB 421 LAGNQLDITTEMFGSSSSS-----ELKSLNLANHKIHSISRSPSDLDNLOQ 468
QY 81 LRLSHNRIOQLDLSYFKFNQDLEYLDLSHNOLOKISCH-----PIVSFRHLD----- 127
DB 469 LRLSHNRIRITTSMTFSNRLRYLDLSHNRILIKILPSALYQLPALDVLHLDHNNLNIID 528
QY 128 ---LSFNDFKALPI-----CKERGNISQNLFLGLSAMKLOKLDLPLAHHLLEYI 174
DB 529 RDAFRSFDLSQSLKLSHNAFRFRSCFELGSIQVHQDLSSNQINEIDIFCIAR----- 582

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```

QY 175 LLDLBNYYIKEMETSLOQLNAKTHLVHPHPSLAIQVN-----ISVNT--LGLQLTN 227
Db 583 --GIRKSLASNSVKE--INRKLQ--DATELTSSIDISHNGIIDVSDAFCECRKLSH 634
QY 228 IKLND-----NOVFIKPLSELTRGSTLNFNLHETWKLVAVFOGIMKPEY 280
Db 635 IKLSNNYIRNLWKGTTRVCIPWISHLT--TCEFTKEHLERTIS----FSYIIVDSQOL 686
QY 281 LNIYNMLT-----IESIREDF-----TYSKTLKALTEHITNOV 316
Db 687 TSFGSLSLSPANNKVDSDIEDGAFENLSLKLIDLSNNPYTWSMSTAFRDLSS--HSISIT 744
QY 317 FLFSQALYTV--FSEKNNIMMLTISDT----- 341
Db 745 NM-AANTGFSPMKFHSRISQSLNISCNKIYELSEKDLAPTRKVALDISHNNLKQISSMA 803
QY 342 --PFIHMLCPHAPSTFFKPLNFQVWFTDSIPEKCTLYKLETLILQKGLKDL--FVVG 396
Db 804 FEPRLIHL-----KOLNVSANPITHLJTHEHIOQLYKL-----YNIPDMARPYOIS 847
QY 397 LMTKMPSELIL--DVSNNLSLEGRHKENCNTWESIVIVLNLSSNNMLTOSVRCLEP-RIK 453
Db 848 SILSLMPLPHITTYVIDIKESALDROFYADTRLLRLHVAAGRNLKYIEVGAAFAATJRGFFVR 907
QY 454 VLDLHSNNIKSVKPOVKLEALQELNVAFNSLTLD--LPQCSF--SLSVLFIIDHSVSHP 510
Db 908 I-EIINSSIEERPSNI--FDPLTGISLILSLSTDNKLTTPNPFGSTVAPAYNQHTIILH- 963
QY 511 SADPFQSCQKRSIKAGNPFQCTGELR--EFVKNIDQVSSVLEGMPSDQYKCDYPESY 567
Db 964 -----SLELKNNPIKCDQCFKMDDFIVUTKFLSDHHSIHDFFDKVECADQGS- 1010
QY 568 RGSPLKDF 575
Db 1011 --SNLESF 1016

```

```

RESULT 4
T13887
clir protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13887
R:Chang, C.; Beachy, P.A.
Mech. Dev. 47, 225-239, 1994
A:Title: Expression of a novel Toll-like gene spans the parasegment boundary and controls
A:Reference number: Z17805; MUID:95151581; PMID:7848870
A:Accession: T13887
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1385 <CHI>
A:Cross-references: UNIPROT:O24591, UNIPARC:UPI000016C024, EMBL:S76155, NID:G913247, PIR
C:Genetics:
A:Cross-references: FlyBase:FBgn0004364
A:Note: clir

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Query Match      6.6%; Score 274; DB 2; Length 1385;
Best Local Similarity 21.6%; Pred. No. 9.1e-10;
Matches 206; Conservative 160; Mismatches 311; Indels 278; Gaps 52;

QY      RGLIHVPDPLDKTKVLMDSQNYIAELQVSMFS--ISELTVLRLSHRIGLDLDSVYKF 98
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      300 KGLHRLLEQL---LVLDLSGNQLTDHHVDNSTFAGLRIRLVLMSSNALRIRGSKTFKE 355
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY      99 NQDLEYLDLSHNOLOKI---SCHPIVSFRHLDLSND-----FKALPI----- 138
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      356 LYLQILDMRNNSIGHIEGAFPLPYNLHTLNLANENRHTIDNRIFNGLVYLTKLTINN 415
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY      139 -----CSEFGNLSQNLGLISAMKLOKLDLPIAHHLSTY-LLDRNRYIKENETESL 191
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      416 LVSIYESAFNCSGLKELDLSNOLTE---VPFAADLSIMLKULDGENOISFFKNYTE 472
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

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QY 192 QILNAKT--LHVFEH-----PTSIPAIQWISVNTLGGCLQINIKYN--DDMCQYFI----- 239
Db 473 ENLQWLTGELRLIDRKIGNITVGMFODLPERLSVLNIAKNRIGSIEBGAFDKXTEIEAIRLD 532
QY 240 -KFLSEL-----TRGSTP--LNFPLNHIETWKCIVRFPQFLW--PKPEYUINYNLTIES 291
Db 533 KKFPLDINGITPATIASLIMLMLSENHL--VN-----FDYAFIBSNLKMIDHG--NYIEA 583
QY 292 -----IREE-----DEFTSK--TYLKALTEIHTNOVL-----FS 320
Db 584 LGNYVKLOEERIVTTLDSASHNRITIEIGAMSVPSNIIEFFINNIIIGQIQANTFVDKTRLA 643
QY 321 QYALY--TYFSEMNIMLTIS-----DTPF----- 343
Db 644 RVDLYANVLISKISNALNVAAPVSAEKVPBEFYLGNPPECCDSMEWIORINNLTTROPH 703
QY 344 -----IHMLCPHA-----PSTPKFLNFTQ----- 362
Db 704 VVDIGNIECLMPHSRSAPLRPLASISADFPYCKTESHCPRCHCEYEQCEBCEYICPENC 763
QY 363 NVFTDSIFE-----KC--STLVKLETLILQKNGLNDLFKVGIMTRKDMBSLEILDVSNLSLE 416
Db 764 SCFHDATWATNIVDQGRDILAALPNRIPQ--DVSDLYLDG--NNMPELEVGHU----- 812
QY 417 SGHKEKNCWTVESTIVLNLSSNMLTDSYFRCLPRRIKYLDSHKIKISVP--KQYVKLEAL 475
Db 813 TGRNRRLAYLNANSLMMLTQNGSLAOLV-----NLRYLHNNKLTALBEGTERFERSLDLL 866
QY 476 QELNVAFNSLIDLDPGCCSFS---SLSVLYIDHNSVSHPSADFPSCQKMRISXKAGDNPFQ 532
Db 867 RELVYHNMLTHISN--ATFEPVLSLEVIKRLNNRIS--SLPHLOYRHSLOGLTIGRANWS 923
QY 533 CTC-----ELAREPVKNIDOVSSSEVLGMPDSYKCYD-----PESYRGSPJK 573
Db 924 CRCQQLBELAQFVSD---NAMVVURDADHDIYCLDAGIKREBELIGNLANGPDC---SDLL 976
QY 574 DFHNSSELSCN-----ITLLIVTIGATMLVLAVTVTSICITYLDLPTWLRWQY 620
Db 977 DNASINISSODLAGGYRLPLLAVALVLIPIFDVLLIIVFVRESVRMLFAHYGR--VCE 1035
QY 621 WTORRRRARBNPLBELQNLQFHAFISYSEHDSAMVSELVPYE--KEDIQICLHERNF 678
Db 1036 -----PREDDGKL--YDAIILHSEQDYFVCNRIABELEHGRRPRLCTIQOQDL 1083
QY 679 VPKGISVENIINTCEKSYKISFYVLSPNFVQSEWCHEYELFEAHNLPHGSGNNLI--LILL 736
Db 1084 PRQASHQ--LVEGARASAKIILVLRNLDLATEWNRIEP---RAAFHESLRGLAGKQVLII 1138
QY 737 EPIQNSIPNKYHKALKALMTORTYLOWPKEKSGKL-----FANIRAPAKMKT 786
Db 1139 E---ETSVSAEABDAVEL---SPYIK--SVPSNNLLTCDRYFEMKLTLYVAIPIEIS 1185

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RESULT 5
T22117
hypothetical protein F43C1.1 - Caenorhabditis elegans
C|Species: Caenorhabditis elegans
C|Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C|Accession: T22117
R|Jasael, B.; Smith, A.
submitted to the EMBL Data Library, December 1994
A|Reference number: Z19519
A|Accession: T22117
A|Status: Preliminary; translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 1-1039 <WIL>
A|Cross-references: UNIPROT:Q09564; UNIPARC:UPI000013BF7A; EMBL:Z46537; PIDD:CAA87056.1
A|Experimental source: clone F43C1
C|Genetics:
A|Gene: CESP:F43C1.1
A|Map position: 3
A|Intons: 83/1; 105/1; 185/3; 283/3; 358/3; 386/1; 438/2; 490/2; 516/3; 609/3; 686/2; 7

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T50850
receptor protein kinase homolog [imported] - soybean
C/Species: Glycine max (soybean)
C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #ext_change 31-Dec-2004
C/Accession: T50850
R/Yamamoto, E.; Karakaya, H.C.; Knap, H.T.
Biochim. Biophys. Acta 1491, 333-340, 2000
A/Title: Molecular characterization of two soybean homologs of Arabidopsis thaliana CLAV
A/Reference number: Z25262
A/Accession: T50850
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-987 <YAM>
A/Cross-references: UNIPROT:Q9M6A7; UNIPARC:UPI00000AC3C7; EMBL:AF197947; PIDN:AAF59906.
C/Genetics:
A/Gene: CLV1B
C/Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat ho

Query Match 5.9%; Score 244.5; DB 2; Length 987;
Best Local Similarity 19.5%; Pred. No. 4.9e-08;
Matches 177; Conservative 121; Mismatches 224; Indels 387; Gaps 42;

QY 45 HVPKDLPLKTKV-LDMQNYIAELQVSDMSFLSELTVRLSHN-----R 87
DB 88 HLPPEIGQLDKLENLTVSQNNLTGVLPKELALTSIKHINISHVFSGHFPGQIILPMTK 147
QY 88 IOLLDL-----SVKFNQDLEYLDLSHN 110
DB 148 LEVLVDYNNFTGPPLELVLEKLYKLDGNYFSGSIPESSYSEK---SLEFSLSTN 204
QY 111 QIQ-KI--SCHPIVSFRHLDSFNDPKALPICKEFENLSQNLFLGSAKKLQKLDLPTA 167
DB 205 SLSGKIPISLSKTKLRKYKLGNNAYEGGIPPEFSMSKLYDSSCNLSG----- 257
QY 168 HHLSYILDLRNYIKENETESLOLN-AKTLHLVFPHTSLPAIQVINSVNTLQGLQLT 226
DB 258 --EIPPSLANLTNL-----DTLFLQINNLTGTI-----PSELISAM---VLSMSL----- 296
QY 227 NIKLNDNQCQVFIKFLSELTRGSTLNTFLNHIETWKLVAVFOGLMKPPEYANITVL 286
DB 297 DLSINDLGEIIPMSF-SQL-RNLTLMNFPQNNLRGS-----VPSPVGLP----- 339
QY 287 TIIESIREDFYTSKTLKALTEHTNQVPLFSQALVTYFSEMMIMMLTISDPFIMH 346
DB 340 -----NLETLQIMDNFSEV 354
QY 347 LCPHAPST--FKPLNFTQNV-----TDSIFE-----KCSITLV 377
DB 355 LPPNIGQNGKLEKFFDVIRKHFGLIPROLCRSGRLQITMITDNFPRGPIRNEIGNCKSLT 414
QY 378 KLETLILQKNGL-KDLFVGMATKDMSELELDVSMSLE-----SGRHKENTWYE 428
DB 415 KIRASNNYLVGVPSGIFK-----LPSTVITIELANNFNGELPREISG-----E 458
QY 429 SIIVANLSSNNMLTDSVFRCLPPIK-----VLDSHSNK-IKSVPOAVKLEALQINYA 481
DB 459 SLGIITLISNNLFSGKI-----PPAKKRLALQTLISLANEFVEIGREAVDLEMLTVNIS 514
QY 482 FNSLIT-----DL-----PGGSSSSLVLIIDHNSVSHSADPF 515
DB 515 GNNLTGPIPTTLTRCVSLTAVDLISRMLEGIKPKGKXNLTDSIFNVSINQSGPVEBI 574
QY 516 QSCQMRISIKAGDNFQCTCELRFEVKNIDV-----SSEVLGEPD---SYKCY 563
DB 575 RMLSLTITLDSNNNF-----IGKVPITGGQFAVFESEKSPAGNPILCTSHSCPN 622
QY 564 PESYSGPLKDFH--MSELSCNITLITVIGATMLVATVLSLCIYDLPWYLRMVCQM 621
DB 623 SSLVDDDLKKRRGPMWSLKSTRVIYVIALGTAALLVATVYMM----- 666
QY 622 TOTRRRARI---PLEELQNLQTHAFISYSEHDSAWKSELVPLEKEDIQICLHERN 677
DB 667 ---RRKKNLAKTWKLTAFOR-LNFYA-----EDVVECLKEEN 700

QY 678 FVP-----GKSIVENINCI----- 692
DB 701 IIGKGAGIVYRGSMPNEDVALIKLVGAGSGRNDYGFQAEIETLCKIRHRIMRLIGV 760
QY 693 --EKSYKSIIVLSPNEVQSEWCH-----YE-----LYFAHN-----LFPH 726
DB 761 SKNETLILLXYEMPNQSLQEMJHGAKGHLKXMEMRKXIVAEAKGICYLHDCSPILHR 820
QY 727 G--SNNLIL 733
DB 821 DVKSNMILL 829

RESULT 8
S42799
garp precursor - human
C/Species: Homo sapiens (man)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 09-Jul-2004
C/Accession: S42799; I37407
R.Birnbaum, D.
Submitted to the EMBL Data Library, July 1993
A/Reference number: S42799
A/Accession: S42799
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-662 <BIR>
A/Cross-references: UNIPROT:Q14392; UNIPARC:UPI000012B0DF
R.Olendorff, V.; Noguichi, T.; delapeyriere, O.; Birnbaum, D.
Cell Growth Differ. 5, 213-219, 1994
A/Title: The GARP gene encodes a new member of the family of leucine-rich repeat-contain
A/Reference number: I37407; MUID:94235567; PMID:8180135
A/Accession: I37407
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-662 <RES>
A/Cross-references: UNIPARC:UPI00012B0DF; EMBL:Z24680; NID:g439295; PIDN:CAA80847.1; PI

C/Genetics:
A/Gene: GDB:GARP; D15833E
A/Cross-references: GDB:433911
A/Map position: 11q13.5-11q14
F:50-73/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F:74-97/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:98-121/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F:150-173/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F:174-197/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F:198-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F:244-265/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F:266-289/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F:316-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F:340-363/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F:364-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F:411-433/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F:444-466/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F:467-514/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F:515-536/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F:537-560/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
F:561-583/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>

Query Match 5.7%; Score 238; DB 2; Length 662;
Best Local Similarity 22.4%; Pred. No. 7.7e-08;
Matches 159; Conservative 91; Mismatches 267; Indels 192; Gaps 29;

QY 17 LMIIVTRIPQSDNEF-AVDKSR-----GLIHVPKDLPLTKVLDMSQNYIAELQVSD 71
DB 9 LALITLGLAAGQNDVPCMDVKXVSCVYLGLQVPSVLPPTETLTDLSGNDLRSLTASP 68
QY 72 MSFLSELTVLRISNRIQLDLISVFKENQDLEYLDLSHNOLOKISC-----HPIVSFRH 125
DB 69 LGFYALRHLDTSTNBIISFLQGAFOALTHTLEHLSLAHRLAMATLASAGIGPVPRTVS 128

F:547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
 F:572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
 F:596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
 F:620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
 F:651-699/Domain: proteoglycan carboxyl-terminal homology <PC3>
 F:708-733/Domain: proteoglycan amino-terminal homology <PA4>
 F:743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
 F:767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
 F:846-890/Domain: proteoglycan carboxyl-terminal homology <PC54>
 F:1028-1061/Domain: EGF homology <EGF2>
 F:1068-1099/Domain: EGF homology <EGF2>
 F:1115-1148/Domain: EGF homology <EGF1>

Query Match 5.6%; Score 233; DB 2; Length 1469;
 Best Local Similarity 18.9%; Pred. No. 4,7e-07;
 Matches 170; Conservative 112; Mismatches 293; Indels 326; Gaps 31;

36 VDKSRKGLIHPKDLPLKTKVLDMSQNYIAELQVSDMSFLSETLVRLSHNRIOQLDLSV 95
 84 VDCSHRGILSVPRKISADVERLELQGNNTLVYETDFQRLTKRLMLQTLNDQIHTERNS 143
 96 FKFNDLEVLDSHQLOKISCHPI--VSFRLDISFDFKALPICKFQNLSQLNPLG 152
 144 FQDLVSLERLDISNNVITTVGRRVFKGQSLRSLQIDNNQITC-----LDEHAFKG 194
 153 LSAAMLQKLDLPIAHLHSLYLLDRLNRYIKENETESLIQILNAKTHLVHPHPSLFAIO 212
 195 L-----VELEILLNNNTLSLPHNF-- 216
 213 VNISVNTLGCTQITNLIKNDNCQVFIKFLSETLRGST-LNFTLNHITTKCLVRFVQ 271
 217 ---GGIGRLALRLSDNPFACDCHLSYLSRFLSATLAVYT-----RCQS--- 259
 212 FLMPKPEVLYNLTITISIREDFYTSKTLKA----- 306
 260 ---PQLKGQNVADL-----HDOEFKCSGLTEHFMEEGARNSCPHPCADGIYDCRE 310
 307 ---LTIHITNQVLFQSOTALYTVSENNIMMLTISDPFIHMLCPHAPSTFKFL- 358
 311 KSLTSVPVTLPPDITDVL-----EON-----FTLELPKSFSSFRRLR 349
 359 -NFTQNVFTDSIFPKCSTLVKLETLTIQKNGIKDL--FVGLMT----- 399
 350 RIDLSNNNISRIAHALSGLKQTLTVLVGKNIKDLPSGVFK-GLGSLRLILNANEISC 408
 400 ---KMPSELTIDVSNLSIES----- 417
 409 IRKDAFRDLHSLSLSLYDNNIQLANGTFDAMKSKWTHLAKNPFICDNLRLWLDLYH 468
 418 ---GRKENCITWESIYVNL----- 434
 469 KNPIETSGARCESPRMHRRIRESREEEFKCSGWEILRKLKSGECRMSDSCPMACHCEGT 528
 435 ---LSSNML-----TDSVPRCLPPRIKVLVDLSNNIKISV- 465
 529 TVDCGRRLKEIPRIPLHTTELLDNDLNGRISSDGLFGRPLHVK-LELGRNQLTGIE 587
 466 PKQVVKLEALQELNAFNSLTDLPG--CGSFSSLSVLLITDHNSVSHPSADFQSCQKMS 523
 588 PNAFEGASHIOELQGENKIKELISNMKFLGHLQTLKTLNLYDQICVMPGSEFHNSLTS 647
 554 IKAGNPQOCCELEAFVKNIDQVSSEVLEGPDSYKCDYPSYSGSLPKDHFMSLGN 583
 648 LNLASNPKNCHLWMAFECVKKKS--LNG--GAARCAPSKVDVQIKDLPHSEFKKS 702
 584 ITLLVITGATMLVLAIVTSLCTIYLDLPWYLRMVCQWOTQRRARANIPLSELQNLQPH 643
 703 SENSEGLGADGYCPSCTCTGVV-----ACSRQLKEIPRGIPAE----- 743
 644 AFISSEHDSAMVKEIPLVLEKEDIQICLHERNFVPGSIYENT--INCISKYSKISFV 701
 744 -----TSEL--YLESNEIEQIHYR-----IRLRSLTRLDSLNNQITTI 780

QY 702 LSPNFQSEWCHYEYELFAHNLFH-----RGSNNLILILEPIFQNSIP-NKYAKLKA 753
 DB 781 LS-NTFAFLTKLSTLIIISYNLQCLQRRALSGNNLRVSLHGNRISMLPFGSFDDLS 839
 QY 754 L 754
 DB 840 L 840

RESULT 11

A36665
 slit protein 1 precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 30-Apr-1991 #sequence revision 30-Apr-1991 #text_change 02-Aug-2002
 C:Accession: A36665, A31640, S13523
 R:Rotberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
 Genes Dev. 4, 2169-2187, 1990
 A:Title: slit: an extracellular protein necessary for development of midline glia and cc
 A:Reference number: A36665; MUID:9109665; PMID:2176636
 A:Accession: A36665
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1480 <ROT>
 A:Cross-references: UNIPARC:UPI0000150FD1; GB:X53959; NID:98614; PIDN:CAA37910.1; PID:98
 R:Rotberg, J.M.; Hartley, D.A.; Walthers, Z.; Artavanis-Tsakonas, S.
 Cell 55, 1047-1059, 1988
 A:Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of
 A:Reference number: A31640; MUID:89077533; PMID:3144436
 A:Accession: A31640
 A:Molecule type: DNA
 A:Residues: 881-1182, 'G', 1185-1404, 'GT', 1463-1464, 'YHA', <RO2>
 A:Cross-references: UNIPARC:UPI000016BD7A; GB:M23543; NID:9340939; PID:9514357
 C:Genetics:
 A:Gene: FLYBase:sl
 A:Cross-references: FLYBase:EBgn0003425
 A:introns: 1351/3
 C:Keywords: alternative splicing; growth factor
 C:Keywords: alternative splicing; growth factor
 F:666-91/Domain: proteoglycan amino-terminal homology <PAH1>
 F:101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
 F:125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
 F:149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F:173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
 F:197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
 F:228-272/Domain: proteoglycan carboxyl-terminal homology <PC51>
 F:288-313/Domain: proteoglycan amino-terminal homology <PAH2>
 F:323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
 F:347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
 F:371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
 F:395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
 F:419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
 F:450-494/Domain: proteoglycan carboxyl-terminal homology <PC52>
 F:512-537/Domain: proteoglycan amino-terminal homology <PAH3>
 F:547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
 F:572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
 F:596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
 F:620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
 F:651-699/Domain: proteoglycan carboxyl-terminal homology <PC53>
 F:708-733/Domain: proteoglycan amino-terminal homology <PAH4>
 F:743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
 F:767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
 F:791-814/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
 F:815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
 F:846-890/Domain: proteoglycan carboxyl-terminal homology <PC54>
 F:1028-1061/Domain: EGF homology <EGF2>
 F:1068-1099/Domain: EGF homology <EGF2>
 F:1115-1148/Domain: EGF homology <EGF1>

Query Match 5.6%; Score 233; DB 2; Length 1480;
 Best Local Similarity 18.9%; Pred. No. 4,7e-07;
 Matches 170; Conservative 112; Mismatches 293; Indels 326; Gaps 31;
 36 VDKSRKGLIHPKDLPLKTKVLDMSQNYIAELQVSDMSFLSETLVRLSHNRIOQLDLSV 95

```

Db      84 VDCSHRGITSVPRKISADVERLELQGNMLTVYETDFQRTGLRMLOLDNQIHTIERN 143
Qy      96 EKNPNODELYLDLSHQLOKISCHP1---VSPHILDSNDFALICKEFGSLQNLFLG 152
Db      144 FQDLVSLERLDISNNVITTVGRRVKGASQSLQLDNNQITC-----LDHAFRG 194
Qy      153 LSAKMLQKLDLPLIAHLHLSYLLDLRNYIYI KENETESQIOLNAKTLHVFHPSTLFAIQ 212
Db      195 L-----VELEILTNNNNLTS:PHNIF--- 216
Qy      213 VNISVNTLGLQTLNKLNDNCQVFIKFLSELTEGST-LNLFNLHLETTWKCLVVRVQ 271
Db      217 ---GGIGRLRALSLSDNPFCDCHLGSLSRFLSATRLAPYT-----RCOS--- 259
Qy      272 FLMPKPVYLYNLYNLTIESIREDEFTYKTLKA----- 306
Db      260 ---BSQLKGQNVAD1-----HDQEFKCSGLTEHAPMECGAENSCHPCRGADGVDCRE 310
Qy      307 ---LTIHITNOVELFSQALYTVFSENNIMMLTISDPTIHLCPHADSTFKPL- 358
Db      311 KSLTSVPTLPPDITDVL-----EQN-----FITELPKSFFSFRRLR 349
Qy      359 -NFTQNVFTDSIFPKCSITLVKLETLIQKNGKDL---FVGLMT----- 399
Db      350 RIDLSNNNISRIAHDALGKQTLVLVGNKIKDLPQGVFK-GLSGLRLILNANEISIC 408
Qy      400 ---KMPSLIEDVGMNSLES----- 417
Db      409 IRKQAFRLHLSLISLYDNNIQLANGTFDAMKSNKTVHLAKNPICDCLRLMADYH 468
Qy      418 ---GRHKENCTWVESIVLVN----- 434
Db      469 KNPITSGARCSPPKMRHRRRIESELREKFKCSWGBELRMKLSGECDMSDCPAMCHCEST 528
Qy      435 ---LSSNML-----TDSVRCPLPPRIKYLDLHNSKIKSY- 465
Db      529 TVDCTGRRLKEIPRDIPLHTTELLINDNELGRISDGLFGRLLPHLYK-LELKRNLQLTGIE 587
Qy      466 PKQVVKLEALQELNANFNSLTLPQ--CSPFSSLSVLIIDHNSVHPSADFPQSOQKMS 523
Db      588 PNAFEGASHIOELQGENKIKESINMKMELGHLQTLKTLNLYDNOISCVMGSEHNLNLS 647
Qy      524 IKAGNPFOCTCELEEFVKNIDOVSEVLEGMWPDYKCDYPSYSGSPKCDPFHMSLSCN 583
Db      648 LNLASNPNQNCNHLMPACVAKKS---LNG--GAARCAPSKADVOIKDLRHPSEFKS 702
Qy      584 ITLLIVTIGATMLVLAIVTSLCIYLDLPWYLRMVCQWOTRRRARNIPLEELQRLNLF 643
Db      703 SENSEGCLGDGYCPSCTCTGTIV-----ACSRNQLKEIPRGIPAE----- 743
Qy      644 AFISISEHDSAMVSELYLEKEDIQICLHERNFPKGSYEENT--INCIEKSYKSIYV 701
Db      744 ---TSEL---YLESNELBQIHYER-----IRHRSRLRLDLSNNQIT 780
Qy      702 LSPNFOSEWCHYEYFAHNLFLH-----GSGNNLILILEPIQNSIP-NKYHKLKA 753
Db      781 LS-NTFANLTKLSTLITISYKLCQCLQRHALSGLNNLRVLSLHGRLISMLPESGFEDLKS 839
Qy      754 L 754
Db      840 L 840

```

RESULT 12

B66234

hypothetical protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #ext_change 31-Dec-2004

C:Accession: B66234

R:Thelodopsis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
 A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A66141; MUID:21016719; PMID:11130712
 A:Accession: B66234
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-921 <STO>
 A:Cross-References: UNIPROT:004517, UNIPARC:UP10000048210, GB:A6005172, NID:g2160189, PI
 C:Genetics:
 A:Map position: 1
 C:Superfamily: Receptor-like protein kinase

```

Query Match      5.5%; Score 230.5; DB 2; Length 921;
                  21.5%; Pred. No. 3.7e-07;
Best Local Similarity 137; Mismatches 317; Indels 175; Gaps 39;
Matches 172; Conservative 137; Mismatch 317; Indel 175; Gap 39;

Qy      50 LPLKTKVLDMSQNYIAELQVDMSEFL-SELTVLRLSHNRIOLDLSVFEKFNODELYLDLS 108
Db      35 LKLMSFPAD-----SNLAVPDSWKLNSEALQLR-----ISLV-----ESLEKSLG 76

Qy      109 HNOLOKI-----SCHPIVSEPHLDLSENDER-ALPICKERGNLSQNLFLGLSANKLOKL 161
Db      77 FNSLSGLIPDLKNC---TSLKYLDLGNLPSGAFPP---EFSINQLOFLYIINNSAFS-- 128

Qy      162 DILPFAHLLH--LSYLLDLRNYIYI KENETESQIOLNAKTLHVFHPSTLFAIQNVISVT 219
Db      129 GVFPWKSIRNATSLVLSLGNPPDADAPFEVVSLSKLSLWLYNSCSISGKIPPAIGD 188

Qy      220 LGCLOLTNKLNDNCQVFIKFLSELTRGSTLNLFTNLHLETTWKCLVRFQFLMPKVE 279
Db      169 L--TELRHLEISDSGLTEIP--SEISKLYLMQELVNNLSLTGL-----PTG 233

Qy      280 YLNIYVLTIE---SIREDEFTYKTKALTEHITNOVELFS-----QT 322
Db      234 FGNLNLITYLDASTVLLQGLSELRLSTNLVSLQGFENE---FSGEIPLEEGEPDLYNL 290

Qy      323 ALYT--VSENNIMMLTISDPTI---HMLCPHAP-----STPKFLNFTQNVFTDSIF 370
Db      291 SLVTKLTLGSPQGGSLADPDFIDASENLTLGPPIPPMCKKNGKAKALLQNNLTGISIP 350

Qy      371 EKCSITLVLETLIQKNGKDLFKVGLMTKMPSEILDVSNLSSEGRHKENCTWVESI 430
Db      351 ESYANCLTLQFRVSENNLNGTVPAGLM--GLPKLEITDIENNPF--GPITADINKGML 407

Qy      431 VLNLSNMLTDSVRCPLPPRI-----KVLDSHNSKIK-SVPKQVVKLEALQELNVAFN 483
Db      408 GALYVGFPKLSD-----LPBEIGDTESLTLYKVELANNRRFTGKIPSGIKLGLSLKMSQN 463

Qy      484 SLT-DLP-GCGSFSSLVLIIDHNSVHPSADFPQSOQKMSIKAGDNP--QCTCELE 539
Db      464 GFSGEIPDSIGSCMSLVNNAQNSISEIPHTLQSLPTLALNLSDNKLISGRIPESLSS 523

Qy      540 FVKNIIDOVSEVLEGMWPDYKCDYPSYSGSP-----LKDPH-----MSELSCNITLL 587
Db      524 LRLSLDLSNNRLSRIPLSLSTYNGSPNGDGLCSTTIKSNRRICINSRSHGDRRVVL 583

Qy      588 IVTIGATMLVLAIVTSLCIYLDLPWYLRMVCQWOTRRRARNIPLEELQRLNLFAPIS 647
Db      584 CIVFG-----LILILASLVFL---YLKKT-----EKKEGRSL----- 613

Qy      648 YSEHDSAMVSELYLEKEDIQICLHERNFP-----PKSIEVENTINC-- 691
Db      614 --KHESWSIKSPRKMSTFEDDIIIDIKENLIGRGCGDYVRVVLGDGEVAVKHIRCS 671

Qy      692 IEKSYKSIY-VLSPNFOSEWCHYEY---FAHNLF---HEGNNLILILEPIQNSIP 742
Db      672 TOKNFSAMPILTERGSKETETEVQTLISIRHLNVKLYCSITSDDSLVETLPLNG 731

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Db 280 MGTNRFHGKIPASVANASHLTVIQYGNLFSGIITSGRGLNLTLYIMRNLFQTRRQD 339
Qy 233 DNCQVFIKFLSELSTLTNLTNHIETTWKCLVRVFOFLMPKREVEYLINVTIISI 292
Db 340 D-----WQFIDLTNCSKIQ--TLNLGEN-----LGGV 366
Qy 293 REEDFTYKTTIK--ALTIEHTNOVFLFSQALYTFSENNIMLTISDTPFIHMLCPH 350
Db 367 LPNSFSNLTSTLSFLALEINKITGSI-----PKDIGNLIGLOHLYLCNNFRGSL-PS 418
Qy 351 APSTKFLNFT---ONVFTDSIFEKCSLTIVKLETLILQKN-----GLKDLFKYG 396
Db 419 SLGRILKNLGIILAYENNSGSIPLAIGNTELTNLTGINKESGMIPTLTSLNLTLSIG 478
Qy 397 LMTKDM---PS-----LEI-LDVSNNSL-----SGRHK 421
Db 479 LSTNNLSGPISBELNIOQLTSLIMINVSKNLLEGSIPQELGHLKNLVEFHAEENRSLGKIP 538
Qy 422 ENCTWVESIVIVINLTSSNMTDSVFRCLP--PRIKVLDSNKKIK--SVPKQVYKLEALOEL 478
Db 539 NTLGDCQLRLRYLYLQNNLTSGSIPALGQLKGLFTLDSNNLTSGQIPSLADITMLHSL 598
Qy 479 NVAFNLSL-DLRGCSFSSSLVLIIDHNSVSHPSADFPSCQKMSIKAGDNPQCTCEL 537
Db 599 NLFSNSFVGEVPTTGAFAAAGSISIQN-----626
Qy 538 REFVNINQVSEVLEGMPSYK--CDYPSYRSGPLKDFHMSLSCNITLLIYIGAT 594
Db 627 -----AKLGGIPDLHLPRCCPLENRKHP-----VLISVSLAA 663
Qy 595 MLVLAVTSLICLYDLPMYLRMVCQWTQTRRRARNIPLEELQRLQHFATISYS----- 649
Db 664 LAIIS-----SLYLLITWHR-----TKGAPS-----RTSMKGHPVSYSQLVKA 704
Qy 650 -----EHDNAVKSELVYLEKEDQLC-----LHERNF 678
Db 705 TDGFAPNMLLSSGSGSYGKGLNTQDHVAVKVLKLENPKALKSFTABCEALRNMHNRNL 764
Qy 679 VPGKSVENIINCIEKSYKSIPLSPNFQSEWCHEY 715
Db 765 VKIVTICSSIDNRGNDFAIVDFMPNGSLDEMIHPE 801

RESULT 15
T07015
CF-4A protein - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T07015
R:Takken, F.L.; Schipper, D.; Nijkamp, H.J.; Hill, J.
Plant J. 14, 401-411, 1998
A>Title: Identification and De-tagged isolation of a new gene at the Cf-4 locus of tomato
A:Reference number: Z15863; MUID:98335213; PMID:9670557
A:Accession: T07015
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-855 <TAK>
A:Cross-references: UNIPROT:O50024; UNIPARC:UPI000009FC28; EMBL:Y12640; NID:e1289424; PI
A:Experimental source: strain Cf-4; isolate MM-Cf-4
C:Genetics:
A:Gene: Cf-4A
A:Map position: 1

Query Match 5.4%; Score 225; DB 2; Length 855;
Best Local Similarity 23.6%; Pred. No. 7.6e-07;
Matches 123; Conservative 84; Mismatches 176; Indels 138; Gaps 25;

Qy 105 LDIASHNQLQ-----KISCHPIVSFRHLDSFNDFKALPICKRFGNLSQL-----NFL 151
Db 85 LDIGSQIQGKFRHSNLSLQLSNLKRDLDSNDFTGSPISPKGFRSDLTNLDLSDSNFT 144
Qy 152 GISAMKLOKLDLPLAHLHLSTYL-----LDLRNY-YIKENETESLQILNAKTLHLV 202

Db 145 GVISEIHSLSKLAHRLISDOYKLSLGRHNEELLKNTQLREHLSESVNISSTIPSNFS 204
Qy 203 FHPSTLFAIOVNISVNTL-GCL-----QLTNLIKND--DNCQVFIKFLSELTRGS-TLLN 253
Db 205 FHLTNL-----RLSTBELRGVLPBRVFLSNLELLDLSYNPOLVFRPFTTIWNSASIVK 259
Qy 254 FTLNHIETTWKCLVRVFOFLM-----PKPEYILINVTIIESTRDEF 297
Db 260 LYLKRVNIAGN-IPDSFSYLLALHEDLMDVYTNLSGPIKP-----LWNLTVNIESL--DL 310
Qy 298 TYSK-----TTLKALTI--EHITNOVFLFSQALYTFSEM-----331
Db 311 DYNHLEGPIPOLPIREKLSLTIGNNNLDDGGLFSLFSRMTQLEELDFSSNSLTGPIPS 370
Qy 332 -----NIMMLTISDTPFIHMLCPHAPS-----TFKFLNFTQNVFTDSIFEKCSLTAVKL 379
Db 371 NVSGLRNLQSLYLS-----NNLNGSIPSWIPDLPSRLSLDSNNTFSGKIQEFKSKTLSI 426
Qy 380 ETLIQKNGKLDLFRVGLMTKDMPSLELIDVSNLSGSGRHKENCTWVESIVYLNLTSSNM 439
Db 427 VT--LKQNLGPIPNLSLNGE--SLQPLDSHNNI--SGHISSSICNKLIMVLDLGSNN 481
Qy 440 LTDVFRCLPFR-----IKVLDSNKKIK--SVPKQVYK 471
Db 482 LEGTIPQCVBERNEVLSHLDSNNRLSGTITWTSIGSPRAISLHGKLTGKVRSLIN 541
Qy 472 LEALOELNVAFNSLTD-LPG--CGSFSLSVLIIIDHNSVSHP 510
Db 542 CKYLLTLDLGNQLNDTFPNMLGYLSQKILSLRNSKLGHP 582

Search completed: June 2, 2006, 22:54:07
Job time : 31 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 2, 2006, 22:52:45 ; Search time 107 Seconds
(without alignments)
3401.348 Million cell updates/sec

Title: US-10-732-796a-12

Perfect score: 4154

Sequence: 1 MTKDKPIVSKSFHFCVLMII.....IPAAFMKLTLYENNIVKVS 796

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_8:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	4154	100.0	796	ADP56660	Adp56660 Human Tol
2	4154	100.0	796	ADP48601	Adp48601 Human Tol
3	4154	100.0	796	ADU23189	Adu23189 Human Tol
4	4149	99.9	796	AAE16109	AAe16109 Human DNA
5	4149	99.9	796	ADU23188	Adu23188 Human Tol
6	4149	99.9	796	ADU23190	Adu23190 Human Tol
7	4149	99.9	796	ADU23197	Adu23197 Murine To
8	4143	99.7	796	AAE16108	AAe16108 Human DNA
9	4048	97.4	780	AAU25469	AAu25469 Human mdd
10	4021	96.8	781	AAU23197	AAu23197 Murine To
11	3144.5	75.7	795	ADU23195	ADu23195 Murine To
12	3144.5	75.6	806	AAE16108	AAe16108 Human DNA
13	3139.5	75.6	806	AAE16108	AAe16108 Human DNA
14	3139.5	75.6	806	AAE16108	AAe16108 Human DNA
15	3139.5	75.6	806	AAE16108	AAe16108 Human DNA
16	2830	68.1	786	AAE16108	AAe16108 Human DNA
17	2830	68.1	786	AAE16108	AAe16108 Human DNA
18	2830	68.1	786	AAE16108	AAe16108 Human DNA
19	2830	68.1	786	AAE16108	AAe16108 Human DNA
20	2830	68.1	786	AAE16108	AAe16108 Human DNA
21	2830	68.1	786	AAE16108	AAe16108 Human DNA
22	2830	68.1	786	AAE16108	AAe16108 Human DNA
23	1905.5	45.9	811	AAE16108	AAe16108 Human DNA

24	1905.5	45.9	811	3	AAE16108	Membrane-
25	1905.5	45.9	811	4	AAU29230	Human PRO
26	1905.5	45.9	811	4	AAE16108	Human PRO
27	1905.5	45.9	811	5	AAE16108	Human DNA
28	1905.5	45.9	811	6	ABU58606	Human PRO
29	1905.5	45.9	811	6	ABU58606	Human PRO
30	1905.5	45.9	811	6	ABU58606	Human PRO
31	1905.5	45.9	811	6	ABU58606	Human PRO
32	1905.5	45.9	811	6	ABU58606	Human PRO
33	1905.5	45.9	811	6	ABU58606	Human PRO
34	1905.5	45.9	811	6	ABU58606	Human PRO
35	1905.5	45.9	811	6	ABU58606	Human PRO
36	1905.5	45.9	811	6	ABU58606	Human PRO
37	1905.5	45.9	811	6	ABU58606	Human PRO
38	1905.5	45.9	811	6	ABU58606	Human PRO
39	1905.5	45.9	811	6	ABU58606	Human PRO
40	1905.5	45.9	811	6	ABU58606	Human PRO
41	1905.5	45.9	811	6	ABU58606	Human PRO
42	1905.5	45.9	811	6	ABU58606	Human PRO
43	1905.5	45.9	811	6	ABU58606	Human PRO
44	1905.5	45.9	811	6	ABU58606	Human PRO
45	1905.5	45.9	811	6	ABU58606	Human PRO

ALIGNMENTS

RESULT 1
ID ADP56660 standard; protein; 796 AA.
XX
AC ADP56660;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human Toll-like receptor TLR6 protein - SEQ ID 12.
XX
KW expression system; Toll-like receptor; TLR6; immune response modifier;
KW IRM; cancer; gene therapy; human; receptor.
XX
OS Homo sapiens.
XX
PN WO2004053057-A2.
XX
PD 24-JUN-2004.
XX
PF 31-OCT-2003; 2003WO-US034563.
XX
PR 11-DEC-2002; 2002US-0432651P.
XX
XX (MINN) 3M INNOVATIVE PROPERTIES CO.
XX
XX Gupta SK, Ghosh TK, Pink JR;
XX
XX WPI: 2004-468833/44.
XX
XX N-PSDB; ADP56659.
XX
PT New expression system comprising a first nucleic acid sequence that
PT encodes a Toll-like receptor (TLR), useful for preparing a composition
PT comprising TLR agonist for treating e.g., cancer.
XX
PS Claim 4; SEQ ID NO 12; 69pp; English.
XX
XX The invention relates to a novel expression system comprising a first
XX nucleic acid sequence that encodes a Toll-like receptor (TLR) operably
XX linked to a first expression control sequence and a second nucleic acid
XX sequence that encodes a reporter. TLRs are immune response modifiers
XX (IRMs). The expression system of the invention may be useful for
XX preparing a composition comprising the TLR agonist for treating cancer,
XX possibly via gene therapy. The current sequence is that of the human Toll
XX -like receptor TLR6 protein (SEQ ID 12) of the invention.
SQ Sequence 796 AA;

Query Match 100.0%; Score 4154; DB 8; Length 796;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MTKDKEPIVKSFFHVCMLIIIVGTRIOFSDGNEFVADSKRGLHVPKDLPLKTVLDM 60
DB 1 MTKDKEPIVKSFFHVCMLIIIVGTRIOFSDGNEFVADSKRGLHVPKDLPLKTVLDM 60
QY 61 QNYIAELQVSDMSFLSELTVLRLSHNRIOQLDLSVFKENODLEYLDLSHNOLOKISCHPI 120
DB 61 QNYIAELQVSDMSFLSELTVLRLSHNRIOQLDLSVFKENODLEYLDLSHNOLOKISCHPI 120
QY 121 VSFRLDLSFNDFKALPICKERGNLSQNLFLGLSAMKLOKDLPLIAHLHSYILLDRN 180
DB 121 VSFRLDLSFNDFKALPICKERGNLSQNLFLGLSAMKLOKDLPLIAHLHSYILLDRN 180
QY 181 YIKENETESLOILNAKTLHLVHFPTSLFAIOVNISVNTLGCLQLTNKKANDNCQVFX 240
DB 181 YIKENETESLOILNAKTLHLVHFPTSLFAIOVNISVNTLGCLQLTNKKANDNCQVFX 240
QY 241 FLSELTRGSTLTNFTLNHIEETWKCLVRFQFLMKPVEYININVLTIIESIREDFYTS 300
DB 241 FLSELTRGSTLTNFTLNHIEETWKCLVRFQFLMKPVEYININVLTIIESIREDFYTS 300
QY 301 KTTLKALTIETHTNOVFLFSQALTYVSENNIMMLTISDTPFIHMLCPHAPSTFKFLNF 360
DB 301 KTTLKALTIETHTNOVFLFSQALTYVSENNIMMLTISDTPFIHMLCPHAPSTFKFLNF 360
QY 361 TQNVFTDSIFEKCSFLVKLETLILQKNGIKDIFKVGMLTKMDPSLEILDVSNLSGSRH 420
DB 361 TQNVFTDSIFEKCSFLVKLETLILQKNGIKDIFKVGMLTKMDPSLEILDVSNLSGSRH 420
QY 421 KENCWVSIIVNLSSNMLTDSVRCLEPBRITKVLDSHNRKTSVPKQVVKLEALQELNV 480
DB 421 KENCWVSIIVNLSSNMLTDSVRCLEPBRITKVLDSHNRKTSVPKQVVKLEALQELNV 480
QY 481 AFNSITLDEPGCGSFSSLSVLIIIDHNSVSHPSADFQSCQKMSIRAGDNPFQCTCELRF 540
DB 481 AFNSITLDEPGCGSFSSLSVLIIIDHNSVSHPSADFQSCQKMSIRAGDNPFQCTCELRF 540
QY 541 VKNIDQVSSEVLKGPDSYKCDYPPSYRSGPLKDFHMSLSCNITLLITTTGATMLVLAV 600
DB 541 VKNIDQVSSEVLKGPDSYKCDYPPSYRSGPLKDFHMSLSCNITLLITTTGATMLVLAV 600
QY 601 TTTSLCTYLDLPWYLRMVCQOTQTRRARNIPLEBELQRLQPHAFISYSEHDSAWKSEL 660
DB 601 TTTSLCTYLDLPWYLRMVCQOTQTRRARNIPLEBELQRLQPHAFISYSEHDSAWKSEL 660
QY 661 VPLYEKEDIQICLHERNFVPGKSIENINICIEKYSKIFVLSPNFVQSEWCHYELYPFH 720
DB 661 VPLYEKEDIQICLHERNFVPGKSIENINICIEKYSKIFVLSPNFVQSEWCHYELYPFH 720
QY 721 HNLPHGSSNNLLILILEPIPNKHYKALKALMTORTYLOWPEKSKRGIFMANIRAA 780
DB 721 HNLPHGSSNNLLILILEPIPNKHYKALKALMTORTYLOWPEKSKRGIFMANIRAA 780
QY 781 FNMKLTLTENNVDKS 796
DB 781 FNMKLTLTENNVDKS 796

RESULT 2
ADP48601 standard; protein; 796 AA.
ADP48601;
ADP48601;
09-SEP-2004 (first entry)
Human Toll-like receptor 6 protein SEQ ID NO:12.
KW Toll-like receptor; TLR; human; detection; identification; TLR agonist;

```

```

KW TLR antagonist; Toll like receptor 6; TLR6; chromosome 4.
XX
XX Homo sapiens.
XX
XX WO2004053452-A2.
XX
XX 24-JUN-2004.
XX
XX 31-OCT-2003; 2003WO-US034554.
XX
XX 11-DEC-2002; 2002US-0432650P.
XX
XX (MINN) 3M INNOVATIVE PROPERTIES CO.
XX
XX Gupta SK, Ghosh TK, Fink JR;
XX
XX WPI: 2004-468955/44.
XX
XX N-PSDB; ADP48600.
XX
XX
XX Detecting activation of Toll-like receptors (TLR) for identifying a TLR
XX agonist or antagonist, comprises providing a cell culture comprising
XX cells transfected with a sequence encoding a reporter.
XX
XX Claim 8; SEQ ID NO 12; 78bp; English.
XX
XX The present invention describes a method for detecting activation of a
XX Toll-like receptor (TLR) in a cell. The method comprises: (a) providing a
XX cell culture comprising cells transfected with a nucleic acid sequence
XX that encodes a reporter that (i) generates a detectable signal when the
XX reporter is expressed and the cell is exposed to conditions for
XX generating the detectable signal, and (ii) is operably linked to an
XX expression control sequence that is induced by activation of a TLR and
XX comprises a cytokine promoter, a chemokine promoter, a co-stimulatory
XX marker promoter, or a defensin promoter; (b) exposing the cell culture to
XX a compound that activates a TLR; (c) providing conditions for generating
XX the detectable signal, and (d) detecting the detectable signal. Also
XX described: (1) a method of identifying a TLR agonist or antagonist; (2) a
XX TLR agonist or antagonist identified by the method of (1); and (3) a
XX pharmaceutical composition comprising a TLR agonist or antagonist
XX identified by the method of (1) and a pharmaceutical salt. The methods
XX are useful for detecting activation of a TLR in a cell and for
XX identifying TLR agonist or antagonist. The present sequence represents a
XX human TLR6 which is used in the exemplification of the present invention.
XX The human TLR6 gene is located on chromosome 4, more specifically to
XX 4p14.
XX
XX Sequence 796 AA;
XX
XX
XX Query Match 100.0%; Score 4154; DB 8; Length 796;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MTKDKEPIVKSFFHVCMLIIIVGTRIOFSDGNEFVADSKRGLHVPKDLPLKTVLDM 60
DB 1 MTKDKEPIVKSFFHVCMLIIIVGTRIOFSDGNEFVADSKRGLHVPKDLPLKTVLDM 60
QY 61 QNYIAELQVSDMSFLSELTVLRLSHNRIOQLDLSVFKENODLEYLDLSHNOLOKISCHPI 120
DB 61 QNYIAELQVSDMSFLSELTVLRLSHNRIOQLDLSVFKENODLEYLDLSHNOLOKISCHPI 120
QY 121 VSFRLDLSFNDFKALPICKERGNLSQNLFLGLSAMKLOKDLPLIAHLHSYILLDRN 180
DB 121 VSFRLDLSFNDFKALPICKERGNLSQNLFLGLSAMKLOKDLPLIAHLHSYILLDRN 180
QY 181 YIKENETESLOILNAKTLHLVHFPTSLFAIOVNISVNTLGCLQLTNKKANDNCQVFX 240
DB 181 YIKENETESLOILNAKTLHLVHFPTSLFAIOVNISVNTLGCLQLTNKKANDNCQVFX 240
QY 241 FLSELTRGSTLTNFTLNHIEETWKCLVRFQFLMKPVEYININVLTIIESIREDFYTS 300
DB 241 FLSELTRGSTLTNFTLNHIEETWKCLVRFQFLMKPVEYININVLTIIESIREDFYTS 300
QY 301 KTTLKALTIETHTNOVFLFSQALTYVSENNIMMLTISDTPFIHMLCPHAPSTFKFLNF 360

```



```

|||||
Db KTTLKALTIETHTNQVFLFSQTAlyTVFSENNIMMLTISDTPFIHMLCPHASTFKFLNF 360
Qy 361 TONVFTDSIFEKCSLTIVKLETLIILOKNGKDLFKVGLMTKMPSEIILDVSNNSLESGRH 420
Db 361 TONVFTDSIFEKCSLTIVKLETLIILOKNGKDLFKVGLMTKMPSEIILDVSNNSLESGRH 420
Qy 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPIIKVLDLHSNKIKSVPKQVVKLEALOELNV 480
Db 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPIIKVLDLHSNKIKSVPKQVVKLEALOELNV 480
Qy 481 AFNSITDLPFGCGSFSSLSVLIIDHNSVSHPSADFPQSCQKMSIKAGDNPFQCTCELREF 540
Db 481 AFNSITDLPFGCGSFSSLSVLIIDHNSVSHPSADFPQSCQKMSIKAGDNPFQCTCELREF 540
Qy 541 VKNIDQVSSEVLEGGPDSYKCDYPSYRGSPLKDFHMSLSGNTLLIVTIGATMLVLAV 600
Db 541 VKNIDQVSSEVLEGGPDSYKCDYPSYRGSPLKDFHMSLSGNTLLIVTIGATMLVLAV 600
Qy 601 TVTSLCTIYLDLPWYLRMVCQMTQTRRRARNIPLEELORNLQPHAFISSEHDSAMVKSSEL 660
Db 601 TVTSLCTIYLDLPWYLRMVCQMTQTRRRARNIPLEELORNLQPHAFISSEHDSAMVKSSEL 660
Qy 661 VPLYEKEDIQICLHERNFVPGKSIIVENIINCIEKSYKSI FVLSPNFVQSEWCHYELYPFH 720
Db 661 VPLYEKEDIQICLHERNFVPGKSIIVENIINCIEKSYKSI FVLSPNFVQSEWCHYELYPFH 720
Qy 721 HNLPHGSGNNLILILEPIPNKHYHKLKALMTQRTYLOWPEKSKRGIFMANIRAA 780
Db 721 HNLPHGSGNNLILILEPIPNKHYHKLKALMTQRTYLOWPEKSKRGIFMANIRAA 780
Qy 781 FNMKLTIVTENNDVKS 796
Db 781 FNMKLTIVTENNDVKS 796

RESULT 3
ADU23189
ID ADU23189 standard; protein; 796 AA.
AC ADU23189;
DT 27-JAN-2005 (first entry)
DE Human Toll-like receptor 6 (TLR6) protein - SEQ ID 81.
KW screening; Toll-like receptor agonist; TLR agonist; TLR6.
OS Homo sapiens.
PN WO2004094671-A2.
PD 04-NOV-2004.
PE 22-APR-2004; 2004MO-US012788.
PR 22-APR-2003; 2003US-0464586P.
PA (COLE-) COLEY PHARM GMBH.
PA (COLE-) COLEY PHARM GROUP INC.
PI Volmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
DR WPI; 2004-795573/78.
XX Identifying agonists of Toll-like receptor (TLR) signaling activity,
XX useful therapeutically or prophylactically, comprises contacting an
XX PT RPM18226 cell that expresses a TLR with a test compound and measuring TLR
XX signaling activity.
XX Discloseure; SEQ ID NO 81; 342pp; English.
XX

```

CC The invention comprises a screening method for identifying agonists of
 CC Toll-like receptor (TLR) signaling activity. The method involves
 CC contacting an RPM18226 cell (that expresses a TLR) with a test compound,
 CC and measuring a test level of TLR signaling activity, where a test level
 CC that is positive is indicative of a test compound that is a TLR agonist.
 CC The method of the invention is useful for identifying agonists of TLR.
 CC The present amino acid sequence represents a TLR protein.

XX
 SQ Sequence 796 AA;

Query Match 100.0%; Score 4154; DB 8; Length 796;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 MTKDEPIVKSPPHPCMLIIIVGTRIQPSDNGEFAVDSKRGILHVPKDLPLKTVLMS 60
Db 1 MTKDEPIVKSPPHPCMLIIIVGTRIQPSDNGEFAVDSKRGILHVPKDLPLKTVLMS 60
Qy 61 QNYIAELOVSQMSFLSELTVLRSLSHNRIOQLDLSVFKFNODLEYDLSHNOLOKISCHPI 120
Db 61 QNYIAELOVSQMSFLSELTVLRSLSHNRIOQLDLSVFKFNODLEYDLSHNOLOKISCHPI 120
Qy 121 VSFRLDLSFNDFKALPICKEFGNLSQNLFLGSLAMKLOKDLPLIAHLHSYILLDRN 180
Db 121 VSFRLDLSFNDFKALPICKEFGNLSQNLFLGSLAMKLOKDLPLIAHLHSYILLDRN 180
Qy 181 YIKENEFESQIINAKTLHLVFHPTSLFAIQVNI SVNTIGLOLTNKKANDNOQVFIK 240
Db 181 YIKENEFESQIINAKTLHLVFHPTSLFAIQVNI SVNTIGLOLTNKKANDNOQVFIK 240
Qy 241 FLSLSTRGSTLNFPLNHIETTKCLVRFQFLMPKPEYINIVYLTIIIESIREDFYIS 300
Db 241 FLSLSTRGSTLNFPLNHIETTKCLVRFQFLMPKPEYINIVYLTIIIESIREDFYIS 300
Qy 301 KTTLKALTIETHTNQVFLFSQTAlyTVFSENNIMMLTISDTPFIHMLCPHASTFKFLNF 360
Db 301 KTTLKALTIETHTNQVFLFSQTAlyTVFSENNIMMLTISDTPFIHMLCPHASTFKFLNF 360
Qy 361 TONVFTDSIFEKCSLTIVKLETLIILOKNGKDLFKVGLMTKMPSEIILDVSNNSLESGRH 420
Db 361 TONVFTDSIFEKCSLTIVKLETLIILOKNGKDLFKVGLMTKMPSEIILDVSNNSLESGRH 420
Qy 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPIIKVLDLHSNKIKSVPKQVVKLEALOELNV 480
Db 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPIIKVLDLHSNKIKSVPKQVVKLEALOELNV 480
Qy 481 AFNSITDLPFGCGSFSSLSVLIIDHNSVSHPSADFPQSCQKMSIKAGDNPFQCTCELREF 540
Db 481 AFNSITDLPFGCGSFSSLSVLIIDHNSVSHPSADFPQSCQKMSIKAGDNPFQCTCELREF 540
Qy 541 VKNIDQVSSEVLEGGPDSYKCDYPSYRGSPLKDFHMSLSGNTLLIVTIGATMLVLAV 600
Db 541 VKNIDQVSSEVLEGGPDSYKCDYPSYRGSPLKDFHMSLSGNTLLIVTIGATMLVLAV 600
Qy 601 TVTSLCTIYLDLPWYLRMVCQMTQTRRRARNIPLEELORNLQPHAFISSEHDSAMVKSSEL 660
Db 601 TVTSLCTIYLDLPWYLRMVCQMTQTRRRARNIPLEELORNLQPHAFISSEHDSAMVKSSEL 660
Qy 661 VPLYEKEDIQICLHERNFVPGKSIIVENIINCIEKSYKSI FVLSPNFVQSEWCHYELYPFH 720
Db 661 VPLYEKEDIQICLHERNFVPGKSIIVENIINCIEKSYKSI FVLSPNFVQSEWCHYELYPFH 720
Qy 721 HNLPHGSGNNLILILEPIPNKHYHKLKALMTQRTYLOWPEKSKRGIFMANIRAA 780
Db 721 HNLPHGSGNNLILILEPIPNKHYHKLKALMTQRTYLOWPEKSKRGIFMANIRAA 780
Qy 781 FNMKLTIVTENNDVKS 796
Db 781 FNMKLTIVTENNDVKS 796

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RESULT 4
 AAE16109

AAE16109 standard; protein; 796 AA.
AAE16109;
26-MAR-2002 (first entry)
Human DNAX Toll like receptor (DTLR) 9 #2.
Human DNAX Toll like receptor; DTLR; therapy; immunological disorder;
interleukin 1; IL-1; screening; immunomodulator.
Homo sapiens.
Key Location/Qualifiers
Peptide 1..31
/label=Signal_peptide
Protein 32..796
/note="Human mature DTLR9"
Region 549..582
/note="Transmembrane segment"
WO200190151-A2.
29-NOV-2001 ✓
23-MAY-2001; 2001WO-US016766.
25-MAY-2000; 2000US-0207558P.
(SCHE) SCHERING CORP.
Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
WPI: 2002-083085/11.
N-PSDB; AAD26300.
New DNAX Toll like receptor (DTLR) proteins, useful for treating
conditions exhibiting abnormal expression of the receptors of their
ligands, particularly abnormalities manifested by immunological
disorders.
Claim 1; Page 76; 297pp; English.
The invention relates to mammalian receptor proteins, e.g., primate,
human DNAX Toll like receptor (DTLR) protein and their corresponding
nucleic acids. The DTLR is useful for treating conditions exhibiting
abnormal expression of the receptors of their ligands. Such abnormality
is manifested by immunological disorders. In particular, the DTLR is
useful for treating various disease or disorders associated with abnormal
expression or abnormal triggering of response to a ligand. The DTLR is
also useful as an immunogen for the production of antisera or antibodies
specific, e.g., capable of distinguishing between other interleukin (IL)-1
receptor family members, for the DTLR or its various fragments. The
purified DTLR can be used to screen monoclonal antibodies or antigen-
binding fragments. The antibodies are useful for screening expression
libraries for particular expression products. These are useful for
detecting or diagnosing various immunological conditions related to
expression of DTLR or cells that express it. The present sequence is
human DTLR9 protein
Sequence 796 AA;
Query Match 99.9%; Score 4149; DB 5; Length 796;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTKDKKEPIVKSFPVCLMIIVGTRIQFSDGNEFAVDKSKRGLIHVPKDLPLKTKVLDWS 60
DB 1 MTKDKKEPIVKSFPVCLMIIVGTRIQFSDGNEFAVDKSKRGLIHVPKDLPLKTKVLDWS 60
QY 61 QNYIYAELOVSDMSFISELTIVLRLSHNRITQLDLISVKNODEYLDLSHNOLOKISCHPI 120
DB 61 QNYIYAELOVSDMSFISELTIVLRLSHNRITQLDLISVKNODEYLDLSHNOLOKISCHPI 120

121 VSPRHLDSFNDPKALPICKFEGNLSQLNFGLSAMKLOKLDLLPIAHLHSYLLDLRN 180
121 VSPRHLDSFNDPKALPICKFEGNLSQLNFGLSAMKLOKLDLLPIAHLHSYLLDLRN 180
QY 181 YIKENETESQIINAKTILHVFHPTSLFAQVNIISVNTIGCLOLTNKLNDNCQVFIK 240
DB 181 YIKENETESQIINAKTILHVFHPTSLFAQVNIISVNTIGCLOLTNKLNDNCQVFIK 240
QY 241 FLSSETRGSTLLNFTLNHIETTWKCLVRVFOFLMPKPEVEYNINVLTIIESIREDFYTS 300
DB 241 FLSSETRGSTLLNFTLNHIETTWKCLVRVFOFLMPKPEVEYNINVLTIIESIREDFYTS 300
QY 301 KTYLKALTIETHTNQVLFPSQTALYTVSENNIMLTIISDTPTIHLCPHAPSTFKPLNF 360
DB 301 KTYLKALTIETHTNQVLFPSQTALYTVSENNIMLTIISDTPTIHLCPHAPSTFKPLNF 360
QY 361 TONVPTDSIFERKSTVYKLETLIIQKNGKDLFVVGMTKMPLELIDVSWNSLESGRH 420
DB 361 TONVPTDSIFERKSTVYKLETLIIQKNGKDLFVVGMTKMPLELIDVSWNSLESGRH 420
QY 421 KENCTWVESIVVLNLSNMLTDSVFRCLPPIKIVLDLSHNRKIKSVKQVVLALQELNV 480
DB 421 KENCTWVESIVVLNLSNMLTDSVFRCLPPIKIVLDLSHNRKIKSVKQVVLALQELNV 480
QY 481 AFNSITDLPGGCSFSSLSVLLIDHNSVSHPSADFPQSCQKRSIKAGDNPQCTCELR 540
DB 481 AFNSITDLPGGCSFSSLSVLLIDHNSVSHPSADFPQSCQKRSIKAGDNPQCTCELR 540
QY 541 VKNIDVSEVLEGPDSYKCDYPSYRGSPLKDFHMSSESCNTLLIVTIGATMLVAV 600
DB 541 VKNIDVSEVLEGPDSYKCDYPSYRGSPLKDFHMSSESCNTLLIVTIGATMLVAV 600
QY 601 TVTSICTYLDLPWYLRMCQMTQTRRRARNIPLELOQNLQPHAFISSEHDSAMVXSEL 660
DB 601 TVTSICTYLDLPWYLRMCQMTQTRRRARNIPLELOQNLQPHAFISSEHDSAMVXSEL 660
QY 661 VPYLEKEDIQICLHERNFVPGKSIIVENIINCIEKSYKSIYVLSNPFVQSEWCHYELFAH 720
DB 661 VPYLEKEDIQICLHERNFVPGKSIIVENIINCIEKSYKSIYVLSNPFVQSEWCHYELFAH 720
QY 721 HNLPHGSGNNLILILEPIPNQSI PNKYHKLKALMTQRTYQWPEKSKRGLFWANIRAA 780
DB 721 HNLPHGSGNNLILILEPIPNQSI PNKYHKLKALMTQRTYQWPEKSKRGLFWANIRAA 780
QY 781 FNMKLTIVTENNDVKS 796
DB 781 FNMKLTIVTENNDVKS 796
RESULT 5
ADU23188
ID ADU23188 standard; protein; 796 AA.
ADU23188;
AC ADU23188;
XX 27-JAN-2005 (first entry)
DT Human Toll-like receptor 6 (TLR6) protein - SEQ ID 80.
XX screening; Toll-like receptor agonist; TLR agonist; TLR6.
KW Homo sapiens.
OS Homo sapiens.
XX WO2004094671-A2.
XX 04-NOV-2004.
PD 22-APR-2004; 2004WO-US012788.
XX 22-APR-2003; 2003US-0464586P.
PR 22-APR-2003; 2003US-0464586P.
XX

PA (COLE-) COLEY PHARM GMBH.
PA (COLE-) COLEY PHARM GROUP INC.
XX
XX
PI Vollmer J, Jurk M, Lipford GB, Schetter C, Forebach A, Krieg AM,
XX
XX WPI; 2004-795573/78.
DR
XX
XX Identifying agonists of Toll-like receptor (TLR) signaling activity,
PT useful therapeutically or prophylactically, comprises contacting an
PT RPM18226 cell that expresses a TLR with a test compound and measuring TLR
PT signaling activity.
XX
XX
PS Disclosure; SEQ ID NO 80; 342pp; English.
XX
XX The invention comprises a screening method for identifying agonists of
CC Toll-like receptor (TLR) signalling activity. The method involves
CC contacting an RPM18226 cell (that expresses a TLR) with a test compound,
CC and measuring a test level of TLR signalling activity, where a test level
CC that is positive is indicative of a test compound that is a TLR agonist.
CC The method of the invention is useful for identifying agonists of TLR.
XX The present amino acid sequence represents a TLR protein.
XX
XX Sequence 796 AA;
XQ

Query Match	99.9%	Score 4149;	DB 8;	Length 796;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 795; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	MTKXKEPILVKSHPFACLMIIIVGTHIQESDNGEPAVDKSRGIIHVPKOLPLTKTYLWMS	60
Db	1	MTKXKEPILVKSHPFACLMIIIVGTHIQESDNGEPAVDKSRGIIHVPKOLPLTKTYLWMS	60
Qy	61	QNYIAELQVSDMSFLSELTVLRLSNHRIOQLDLVSFKFNQDLEYLDLSHNQLOKISCHPI	120
Db	61	QNYIAELQVSDMSFLSELTVLRLSNHRIOQLDLVSFKFNQDLEYLDLSHNQLOKISCHPI	120
Qy	121	VSFRRLDLSFNDFKALPICKERGNISQNLFLGJSAMKLOKDLPLPAHLHSLYLLDEN	180
Db	121	VSFRRLDLSFNDFKALPICKERGNISQNLFLGJSAMKLOKDLPLPAHLHSLYLLDEN	180
Qy	181	YYIKENETESLOILNAKTLHLVHPPTSLPAIOWNISVNTLGCQJOLNIIKLANDNCOVFLK	240
Db	181	YYIKENETESLOILNAKTLHLVHPPTSLPAIOWNISVNTLGCQJOLNIIKLANDNCOVFLK	240
Qy	241	FLSELTRGSTLLNFTLNHIETTKCLVRFQELMPKPYEYLNIMLTIIIESIREEDFTYS	300
Db	241	FLSELTRGPTLLNFTLNHIETTKCLVRFQELMPKPYEYLNIMLTIIIESIREEDFTYS	300
Qy	301	KTLTKALTIETHTNQVPLFSQALATTVBSBNIMIMLTISDTPRIHMLCPHA8STPFELNF	360
Db	301	KTLTKALTIETHTNQVPLFSQALATTVBSBNIMIMLTISDTPRIHMLCPHA8STPFELNF	360
Qy	361	TQNVETDSIFEKCSITLVKLETLILOKNGJLDFPKYGLMTKMDPSLEIILDVSNMSLESGRH	420
Db	361	TQNVETDSIFEKCSITLVKLETLILOKNGJLDFPKYGLMTKMDPSLEIILDVSNMSLESGRH	420
Qy	421	KENCTWESIVVLNLSNNMLTDSVFRCLPBPRIKVDLDHSNKKISVPKQYVVKLEALOELNV	480
Db	421	KENCTWESIVVLNLSNNMLTDSVFRCLPBPRIKVDLDHSNKKISVPKQYVVKLEALOELNV	480
Qy	481	AFNSLTDLPGGSPFSSLSVLIIDHNSVSHPSADFPQSCQKMSIKYAGNDMPFOCTCELRFE	540
Db	481	AFNSLTDLPGGSPFSSLSVLIIDHNSVSHPSADFPQSCQKMSIKYAGNDMPFOCTCELRFE	540
Qy	541	VKNIDQVSESVLEGPMPDSYKCDYPESYRGSPLKDFHMSLSNCNITLLIYVITGATMLVLAV	600
Db	541	VKNIDQVSESVLEGPMPDSYKCDYPESYRGSPLKDFHMSLSNCNITLLIYVITGATMLVLAV	600
Qy	601	TVTSLCTIYLDLPWYLRBMVCOMQOTPRRANRINPLEBELORULOFPAAFISYSEHDSAMWKSEL	660
Db	601	TVTSLCTIYLDLPWYLRBMVCOMQOTPRRANRINPLEBELORULOFPAAFISYSEHDSAMWKSEL	660
Qy	661	VPEYKEBIDQICLHERNFPKGSIAVENIINCIEKSYSKIFVLSPNFVQSEWCHEYELFYAH	720

Db	661	VPLEKEDIQICLHERNFVPGKSIYENINCLSEKSYKSI	PVLSNPFQSEMCHELTYFAH	720
Qy	721	HNLFHSGSNLLILILEPIPNQKHYKALKMTORTYLOMPKEXSKGGLFWANIRAA		780
Db	721	HNLFHSGSNLLILILEPIPNQKHYKALKMTORTYLOMPKEXSKGGLFWANIRAA		780
Qy	781	FNMKLTLYTENNDDYS	796	
Db	781	FNMKLTLYTENNDDYS	796	

RESULT 6
ADU23190
ID ADU23190 standard; protein; 796 AA.

AC	ADD23190;	
XX	27-JAN-2005	(first entry)
DT		
XX	Human Toll-like receptor 6 (TLR6)	protein - SEQ ID 82.
DE		
XX	screening; Toll-like receptor agonist; TLR agonist; TLR6	
FW		

OS Homo sapiens.
XX
PN WO2004094671-A2.

PD	04-NOV-2004.
XX	
PF	22-APR-2004; 2004WO-US012788.

PR 22-APR-2003; 2003US-0464586P.
PR 22-APR-2003; 2003US-0464588P.

PA (COLE-) COLEY PHARM GMBH.
PA (COLE-) COLEY PHARM GROUP INC.

PI Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM,
XX
DR WPI; 2004-795573/78.

PT Identifying agonists of Toll-like receptor (TLR) signaling activity,
PT thermotactically or proprioactively, comprises contacting an
PT RMI826 cell that expresses a TLR with a test compound and measuring TLR
PT signaling activity.

PS Disclosure; SEQ ID NO 82; 342pp; English.

CC The invention comprises a screening method for identifying agonists of
CC Toll-like receptor (TLR) signalling activity. The method involves
CC contacting an RPMI8226 cell (that expresses a TLR) with a test compound,
CC and measuring a test level of TLR signalling activity, where a test level
CC that is positive is indicative of a test compound that is a TLR agonist.
CC The method of the invention is useful for identifying agonists of TLR.
CC The present amino acid sequence represents a TLR protein.

SQ Sequence 796 AA;

Query Match	99.9%	Score 4149;	DB 8;	Length 796;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 795; Conservative	0;	Mismatches	1;	Gaps 0

QY
I MTKDKEIVKSFHFVCLMIIIGTRIQSDGNEFAVDKSKRGLHVPKDLPLTKTVLDM 60

61 ONYIAELOVSDMSFLSEITVLRLSHNRIOQLDLSPFKFNODLEYLDLSHNOLOKISCHPI 120

QY 121 VSFPHLDLSENFKALPCKEFGNLSQNLPIGLSAMKLOKLDLPIAHLHLSYLLDLRN 180

```
Db 121 VSRRLDLSFNDKALPICKERFNGISQNLFLGLSAMKLOKDLPLIAHLHSYILLDRN 180
Qy 181 YYIKENETESLOIINAKTLHLVFPHTSLFAIOVNISVNTLGLQLTINIKLNDNCQVFIK 240
Db 181 YYIKENETESLOIINAKTLHLVFPHTSLFAIOVNISVNTLGLQLTINIKLNDNCQVFIK 240
Qy 241 FLSELTGRSTLLNFTLNHIETTWKCLAVRFOPLMPKPEVYININVTIIESIREDDFTYS 300
Db 241 FLSELTGRSTLLNFTLNHIETTWKCLAVRFOPLMPKPEVYININVTIIESIREDDFTYS 300
Qy 301 KTTLKALITEHTITNOVFLFSQALYVFSNNIMMLTISDPFIHMLCPHASTPFIPLNF 360
Db 301 KTTLKALITEHTITNOVFLFSQALYVFSNNIMMLTISDPFIHMLCPHASTPFIPLNF 360
Qy 361 TONVFTDSIFEKCSLTIVKLETLILQKNGKDLFKVGLMTKMPSEILDVSNNSLESGRH 420
Db 361 TONVFTDSIFEKCSLTIVKLETLILQKNGKDLFKVGLMTKMPSEILDVSNNSLESGRH 420
Qy 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPRIKVLDLHSNKIKSVKQVVKLEALQELNV 480
Db 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPRIKVLDLHSNKIKSVKQVVKLEALQELNV 480
Qy 481 AFNSLTDLPGCGSFSSLSVLIIIDHNSVSHPSADPFQSCQKMSIRAGDNPFCCTCELREF 540
Db 481 AFNSLTDLPGCGSFSSLSVLIIIDHNSVSHPSADPFQSCQKMSIRAGDNPFCCTCELREF 540
Qy 541 VNINIOVSEVLEGMPSYKCDYPESYRGSPLKDFHMSLSGNITLLIYTGATMLVLAV 600
Db 541 VNINIOVSEVLEGMPSYKCDYPESYRGSPLKDFHMSLSGNITLLIYTGATMLVLAV 600
Qy 601 TVTSLICIVLDLPWYLRMVCQMTQTRRRANIPLEBIQRLQPHAFISYSEHDSAMVKSSEL 660
Db 601 TVTSLICIVLDLPWYLRMVCQMTQTRRRANIPLEBIQRLQPHAFISYSEHDSAMVKSSEL 660
Qy 720 VPLYLKEDIQICLHERNFVPGKSIYENIINCEKYSKIFVLSPNVQSEMGCHYELFYAH 720
Db 661 VPLYLKEDIQICLHERNFVPGKSIYENIINCEKYSKIFVLSPNVQSEMGCHYELFYAH 720
Qy 721 HNLFFHSGSNLILILEPIQNSIPNKYHKLKALMTQRTYLOMPKESKRGFLFWANIRAA 780
Db 721 HNLFFHSGSNLILILEPIQNSIPNKYHKLKALMTQRTYLOMPKESKRGFLFWANIRAA 780
Qy 781 FNMKLTIVTENNVDVKS 796
Db 781 FNMKLTIVTENNVDVKS 796

RESULT 7
ADX06216
ID ADX06216 standard; protein; 796 AA.
XX
AC ADX06216;
XX
DT 21-APR-2005 (first entry)
XX
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 781.
XX
KW cytosolic; cyclin-dependent kinase; cdk; biomarker.
XX
OS Homo sapiens.
XX
PN WO2005012875-A2.
XX
PD 10-FEB-2005.
XX
PF 29-JUL-2004; 2004MO-US024424.
XX
PR 29-JUL-2003; 2003US-0490890P.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
```

```
DR WPI; 2005-163068/17.
DX N-PSDB; ADX06215.
XX
PT Biomarkers useful for predicting or determining the response of a mammal
PT to a cancer treatment comprising administration of a modulator of cyclin-
PT dependent kinase activity.
XX
PS Claim 5; SEQ ID NO 781; 141dp; English.
XX
CC This invention describes a novel method of predicting or determining
CC whether a mammal will respond or is responding to an anti-cancer agent
CC that modulates cyclin-dependent kinase (cdk) activity. The method
CC comprises measuring the level of one or more biomarkers selected from
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC NO:1246 (Genbank EST W26729) is especially preferred). The method of the
CC invention is utilized in a kit for determining or predicting whether
CC patient would be susceptible or resistant to treatment by an agent
CC modulating cdk activity. The invention also describes a method for
CC utilizing individualized genetic profiles for treating diseases and
CC disorders based on patient's response and molecular level, specialized
CC microarrays comprising the biomarkers described, antibodies directed
CC against the biomarkers and a cell culture model to identify biomarkers.
CC The cdk modulator is preferably N-5-[(5-(1,1-dimethylethyl)-2-
CC oxazolyl)methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
CC tartaric acid salt. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from Wipo at ftp.wipo.int/pub/published.pat.sequences. This
CC sequence represents a biomarker used in the method of the invention.
XX
SQ Sequence 796 AA;
XX
Query Match 99.9%; Score 4149; DB 9; Length 796;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MTKDKPEIVKSFHFCMLIIIVGTIORSDDGEFVADSKRGLHVPDLPKTKVLMS 60
Db 1 MTKDKPEIVKSFHFCMLIIIVGTIORSDDGEFVADSKRGLHVPDLPKTKVLMS 60
Qy 61 QNYIAELQVDSMSFSELTIVLRSLSHNRIOQLDLSYFKNODELYDLDSHNOLOKISCHPI 120
Db 61 QNYIAELQVDSMSFSELTIVLRSLSHNRIOQLDLSYFKNODELYDLDSHNOLOKISCHPI 120
Qy 121 VSRRLDLSFNDKALPICKERFNGISQNLFLGLSAMKLOKDLPLIAHLHSYILLDRN 180
Db 121 VSRRLDLSFNDKALPICKERFNGISQNLFLGLSAMKLOKDLPLIAHLHSYILLDRN 180
Qy 181 YYIKENETESLOIINAKTLHLVFPHTSLFAIOVNISVNTLGLQLTINIKLNDNCQVFIK 240
Db 181 YYIKENETESLOIINAKTLHLVFPHTSLFAIOVNISVNTLGLQLTINIKLNDNCQVFIK 240
Qy 241 FLSELTGRSTLLNFTLNHIETTWKCLAVRFOPLMPKPEVYININVTIIESIREDDFTYS 300
Db 241 FLSELTGRSTLLNFTLNHIETTWKCLAVRFOPLMPKPEVYININVTIIESIREDDFTYS 300
Qy 301 KTTLKALITEHTITNOVFLFSQALYVFSNNIMMLTISDPFIHMLCPHASTPFIPLNF 360
Db 301 KTTLKALITEHTITNOVFLFSQALYVFSNNIMMLTISDPFIHMLCPHASTPFIPLNF 360
Qy 361 TONVFTDSIFEKCSLTIVKLETLILQKNGKDLFKVGLMTKMPSEILDVSNNSLESGRH 420
Db 361 TONVFTDSIFEKCSLTIVKLETLILQKNGKDLFKVGLMTKMPSEILDVSNNSLESGRH 420
Qy 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPRIKVLDLHSNKIKSVKQVVKLEALQELNV 480
Db 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPRIKVLDLHSNKIKSVKQVVKLEALQELNV 480
Qy 481 AFNSLTDLPGCGSFSSLSVLIIIDHNSVSHPSADPFQSCQKMSIRAGDNPFCCTCELREF 540
Db 481 AFNSLTDLPGCGSFSSLSVLIIIDHNSVSHPSADPFQSCQKMSIRAGDNPFCCTCELREF 540
Qy 541 VNINIOVSEVLEGMPSYKCDYPESYRGSPLKDFHMSLSGNITLLIYTGATMLVLAV 600
Db 541 VNINIOVSEVLEGMPSYKCDYPESYRGSPLKDFHMSLSGNITLLIYTGATMLVLAV 600
```

Db 541 VKNIDQVSEVLEGMWDSYKCDYSPESYRSGPLKDFHMSLSGNTLLITVIGATMLVLAV 600
QY 601 TVTSLCTIYDLPMYLRMVCQMTQTRRRARNIPLEELQRLNQLQPHAFISYSEHDSAMWKSSEL 660
Db 601 TVTSLCTIYDLPMYLRMVCQMTQTRRRARNIPLEELQRLNQLQPHAFISYSEHDSAMWKSSEL 660
QY 661 VPYLEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSIFFVLSPNFVQSEWCHEYELYPFAH 720
Db 661 VPYLEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSIFFVLSPNFVQSEWCHEYELYPFAH 720
QY 721 HNLFHEGSSNNLILILLEPIPNQSIIPKXHKLKALMTQRTYLOMPKEKSRGILFWANIRAA 780
Db 721 HNLFHEGSSNNLILILLEPIPNQSIIPKXHKLKALMTQRTYLOMPKEKSRGILFWANIRAA 780
QY 781 FNNKLTIVTENNNDVKS 796
Db 781 FNNKLTIVTENNNDVKS 796

RESULT 8

AA88054
ID AA88054 standard; protein; 796 AA.

XX AA88054;

DT 22-SEP-2000 (first entry)

DE Human Toll-like receptor TLR6 protein.

KW Toll-like receptor; TLR6; human; anti-infectious; treatment; infection;
transcription factor; NF-kappaB; immune response.

XX Homo sapiens.

XX WO200024776-A1.

XX PD 04-MAY-2000.

XX PF 26-OCT-1999; 99WO-JP005917.

XX PR 26-OCT-1998; 98JP-00304110.

XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX PI Akira S. Takeuchi O;

XX DR WPI; 2000-350697/30.

XX DR N-PSDB; AAA39809.

PT Toll-like receptor TLR6 molecule and encoded gene, participating in
signal transduction of initial immune response, applicable e.g. in
treating infections.

PS Claim 1; Page 27-29; 35pp; Japanese.

CC This invention describes a novel toll-like receptor TLR6 which has
anti-infectious activity. The protein and its encoded gene have clinical
use e.g. in treating infections. Toll family receptors are related to
transcription factor NF-kappaB and regulate the expression of various
CC genes participating in the immune response. This sequence represents the
human TLR6 protein which is described in the method of the invention
XX
SQ Sequence 796 AA;

Query Match 99.7%; Score 4143; DB 3; Length 796;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 794; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTKDKEPIKSPFVFCMLIIIVGTRIQFSDGNFADKSGKGLIHVPKDLPLKTKVLNDS 60
Db 1 MTKDKEPIKSPFVFCMLIIIVGTRIQFSDGNFADKSGKGLIHVPKDLPLKTKVLNDS 60
QY 61 QNYIAELQVSDMSFLSELTVLRISHNRQLDLDSVFKFNQDLELYDLISHNOLOKISCHPI 120

Db 61 QNYIAELQVSDMSFLSELTVLRISHNRQLDLDSVFKFNQDLELYDLISHNOLOKISCHPI 120
QY 121 VSPFRHLDSFNDPKALPIKEFGNLSQNLNFGISAMKLOKDLLPFAHLSYIILLDLN 180
Db 121 VSPFRHLDSFNDPKALPIKEFGNLSQNLNFGISAMKLOKDLLPFAHLSYIILLDLN 180
QY 181 YIKENETESLOLNKATLHVPFSLPAIQVNSVNTLGGCLQNLKLNDDNCQVFIK 240
Db 181 YIKENETESLOLNKATLHVPFSLPAIQVNSVNTLGGCLQNLKLNDDNCQVFIK 240
QY 241 FLSLTRGSTLLNFTLNHIETWKCILVRVQFQFMPKRVLYNLNLTIIIESIREEDFTYS 300
Db 241 FLSLTRGSTLLNFTLNHIETWKCILVRVQFQFMPKRVLYNLNLTIIIESIREEDFTYS 300
QY 301 KTKLKALTEHTNQVFLFSQALTYVESENNIMMLTIDTPFIHMLCPHASTFEKLFNF 360
Db 301 KTKLKALTEHTNQVFLFSQALTYVESENNIMMLTIDTPFIHMLCPHASTFEKLFNF 360
QY 361 TQNVFTDSIFEKCSITLVKLETLILQKNGKDI PKVGLMTKDMPSLEILVSNMSLESGRH 420
Db 361 TQNVFTDSIFEKCSITLVKLETLILQKNGKDI PKVGLMTKDMPSLEILVSNMSLESGRH 420
QY 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPIRIKVLDSLHNSKIKSVKQVVKLEALQELNV 480
Db 421 KENCTWVESIVVLNLSNNMLTDSVFRCLPPIRIKVLDSLHNSKIKSVKQVVKLEALQELNV 480
QY 481 AFNSLTDLPGCGSPSSLSVLIIDHNSVSHPSADFFQSCQKMSIKAGDNPFOCTCELRSF 540
Db 481 AFNSLTDLPGCGSPSSLSVLIIDHNSVSHPSADFFQSCQKMSIKAGDNPFOCTCELRSF 540
QY 541 VKNIDQVSEVLEGMWDSYKCDYSPESYRSGPLKDFHMSLSGNTLLITVIGATMLVLAV 600
Db 541 VKNIDQVSEVLEGMWDSYKCDYSPESYRSGPLKDFHMSLSGNTLLITVIGATMLVLAV 600
QY 601 TVTSLCTIYDLPMYLRMVCQMTQTRRRARNIPLEELQRLNQLQPHAFISYSEHDSAMWKSSEL 660
Db 601 TVTSLCTIYDLPMYLRMVCQMTQTRRRARNIPLEELQRLNQLQPHAFISYSEHDSAMWKSSEL 660
QY 661 VPYLEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSIFFVLSPNFVQSEWCHEYELYPFAH 720
Db 661 VPYLEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSIFFVLSPNFVQSEWCHEYELYPFAH 720
QY 721 HNLFHEGSSNNLILILLEPIPNQSIIPKXHKLKALMTQRTYLOMPKEKSRGILFWANIRAA 780
Db 721 HNLFHEGSSNNLILILLEPIPNQSIIPKXHKLKALMTQRTYLOMPKEKSRGILFWANIRAA 780
QY 781 FNNKLTIVTENNNDVKS 796
Db 781 FNNKLTIVTENNNDVKS 796

RESULT 9

AAE16112
ID AAE16112 standard; protein; 780 AA.

XX AAE16112;

DT 26-MAR-2002 (first entry)

DE Human DNAX Toll like receptor (DTLR) 9 #2, alternative version.

KW Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
interleukin 1; IL-1; screening; immunomodulator.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..31

FT Protein /label= Signal_peptide

FT /note="Human mature DTLR9"

FT Misc-difference 176..177

```

FT      /note= "Encoded by CTGGATTTAAGAAATATATATATAAAGAA
FT      AATGACAGCAAGCTACAAATTT"
FT      549..582
FT      Region
FT      /note= "Transmembrane segment"
EN      WO200190151-A2.
XX      29-NOV-2001.
XX      23-MAY-2001; 2001WO-US016766.
XX      25-MAY-2000; 2000US-0207558P.
XX      (SCHE ) SCHERING CORP.
XX      Hardiman GT, Rock FL, Bazan JF, Kastetelein RA, Ho SWK, Liu Y,
XX      WPI; 2002-083085/11.
XX      N-PSDB; AAD26300.
XX      New DNAX Toll like receptor (DTLR) proteins, useful for treating
XX      conditions exhibiting abnormal expression of the receptors of their
XX      ligands, particularly abnormalities manifested by immunological
XX      disorders.
XX      Claim 1; Page 274-276; 297pp; English.
XX      The invention relates to mammalian receptor proteins, e.g., primate,
XX      human DNAX Toll like receptor (DTLR) protein and their corresponding
XX      nucleic acids. The DTLR is useful for treating conditions exhibiting
XX      abnormal expression of the receptors of their ligands. Such abnormality
XX      is manifested by immunological disorders. In particular, the DTLR is
XX      useful for treating various disease or disorders associated with abnormal
XX      expression or abnormal triggering of response to a ligand. The DTLR is
XX      also useful as an immunogen for the production of antisera or antibodies
XX      specific, e.g. capable of distinguishing between other interleukin (IL)-1
XX      receptor family members, for the DTLR or its various fragments. The
XX      purified DTLR can be used to screen monoclonal antibodies or antigen-
XX      binding fragments. The antibodies are useful for screening expression
XX      libraries for particular expression products. These are useful for
XX      detecting or diagnosing various immunological conditions related to
XX      expression of DTLR or cells that express it. The present sequence is
XX      human DTLR3 protein, alternative version. Note: The present sequence SEQ
XX      ID NO 41 is stated to be similar to the sequence shown in page 76
XX      (AAL16109). However these sequences differ at several locations
XX      SQ
XX      Sequence 780 AA;
XX      Query Match          97.4%; Score 4048; DB 5; Length 780;
XX      Best Local Similarity 97.9%; Pred. No. 0;
XX      Matches 779; Conservative 0; Mismatches 1; Indels 16; Gaps 1;
QY      1 MTKDKEPIYKSHFPCVLMIIIVGTRIQFSDGNEFAVDKSKGLIHHPKDLPLKTKYLDMS 60
DB      1 MTKDKEPIYKSHFPCVLMIIIVGTRIQFSDGNEFAVDKSKGLIHHPKDLPLKTKYLDMS 60
QY      61 QNYIAELOVSDMSFISELTVLRSLSHNRIOQLDLVFKFNQDLEYLDLSHNOLOKTSCHPI 120
DB      61 QNYIAELOVSDMSFISELTVLRSLSHNRIOQLDLVFKFNQDLEYLDLSHNOLOKTSCHPI 120
QY      121 VSRHLDLSFNDKALPICKERGNLSQNLFLGLSANKLOKDLPLIAHLHLSTYILLDLRN 180
DB      121 VSRHLDLSFNDKALPICKERGNLSQNLFLGLSANKLOKDLPLIAHLHLSTYILLDLRN 180
QY      121 VSRHLDLSFNDKALPICKERGNLSQNLFLGLSANKLOKDLPLIAHLHLSTYILLDLRN 180
DB      121 VSRHLDLSFNDKALPICKERGNLSQNLFLGLSANKLOKDLPLIAHLHLSTYILLDLRN 180
QY      181 YIKENETESLOIINAKTILHVPHTSLPAIQVNIQVNTLGCQLTNKLNNDNCQVFLK 240
DB      181 YIKENETESLOIINAKTILHVPHTSLPAIQVNIQVNTLGCQLTNKLNNDNCQVFLK 240
QY      177 -----ILNAKTLHVPHTSLPAIQVNIQVNTLGCQLTNKLNNDNCQVFLK 224
DB      177 -----ILNAKTLHVPHTSLPAIQVNIQVNTLGCQLTNKLNNDNCQVFLK 224
QY      241 FLSELTRGSLINPNTLNHLETTWKCLVRVFOFLMPKPVYINLYNTLTIESTREEPFTS 300
DB      241 FLSELTRGSLINPNTLNHLETTWKCLVRVFOFLMPKPVYINLYNTLTIESTREEPFTS 300
QY      225 FLSELTRGSLINPNTLNHLETTWKCLVRVFOFLMPKPVYINLYNTLTIESTREEPFTS 284
DB      225 FLSELTRGSLINPNTLNHLETTWKCLVRVFOFLMPKPVYINLYNTLTIESTREEPFTS 284
QY      301 KTKLALTEIHTNOVFLFSOTALYTVFSEMMIMMLTISDTPFIHMLCPHASTPEKFLNF 360
DB      301 KTKLALTEIHTNOVFLFSOTALYTVFSEMMIMMLTISDTPFIHMLCPHASTPEKFLNF 360

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DB      285 KTKLALTEIHTNOVFLFSOTALYTVFSEMMIMMLTISDTPFIHMLCPHASTPEKFLNF 344
QY      361 TONVFTDSIFEKCSITLVLETLIILOKNGLKDLFKVGLMTKMPSEIILDVSMNSIESGRH 420
DB      345 TONVFTDSIFEKCSITLVLETLIILOKNGLKDLFKVGLMTKMPSEIILDVSMNSIESGRH 404
QY      421 KENCTWVESIVVLNLSNMULTDSVFRCLPPRIKVLIDHSNKIKSVYKQVVKLEALQELNV 480
DB      405 KENCTWVESIVVLNLSNMULTDSVFRCLPPRIKVLIDHSNKIKSVYKQVVKLEALQELNV 464
QY      461 AFNSTLIDPFGGCSFESLSVLIIIDHNSVSHPADPQSCQKRSIYAGNPPQCTCELRKF 540
DB      465 AFNSTLIDPFGGCSFESLSVLIIIDHNSVSHPADPQSCQKRSIYAGNPPQCTCELRKF 524
QY      541 VKNIDQVSEVLEGPDSKYCDYPESYSGSPDKPFHMSLSNTLLIVTIGATMLVLAV 600
DB      525 VKNIDQVSEVLEGPDSKYCDYPESYSGSPDKPFHMSLSNTLLIVTIGATMLVLAV 584
QY      601 TVTSLCIYLDLPWYLRMVCOMTQTRRRARNIPLBELQBNLOPHAFISYSEHDSAMVKSGL 660
DB      585 TVTSLCIYLDLPWYLRMVCOMTQTRRRARNIPLBELQBNLOPHAFISYSEHDSAMVKSGL 644
QY      661 VPYLEKEDIQICLHRNRPVGSIVENIINCIEKSKYSIFVLSPPVQSEWCHVELYFAH 720
DB      645 VPYLEKEDIQICLHRNRPVGSIVENIINCIEKSKYSIFVLSPPVQSEWCHVELYFAH 704
QY      721 HNLPHGSGNNILILILEPIPNKHYKALKMTQRTYLOMPKSKRGFLFMANIRAA 780
DB      705 HNLPHGSGNNILILILEPIPNKHYKALKMTQRTYLOMPKSKRGFLFMANIRAA 764
QY      781 FNMKLTLYTENNDVKS 796
DB      765 FNMKLTLYTENNDVKS 780
RESULT 10
AAU25469
ID AAU25469 standard; protein; 781 AA.
AC AAU25469;
XX
XX 18-DEC-2001 (first entry)
XX
XX Human mddt protein from clone LI:007302.1:2000MAY01.
DE
XX
XX Human; molecules for disease detection and treatment; mddt;
XX Antiartherosclerotic; hepatotropic; antipapillary; cycostatic;
XX immunosuppressive; antidiabetic; antiaslomatic; neuroprotective;
XX osteopathic; antiarthritic; cell proliferative disorder;
XX arteriosclerosis; cirrhosis; psoriasis; cancer; adenocarcinoma;
XX leukemia; breast cancer; autoimmune disorder; AIDS;
XX acquired immunodeficiency syndrome; Addison's disease; diabetes mellitus;
XX asthma; multiple sclerosis; osteoarthritis.
OS Homo sapiens.
PN WO200162922-A2.
XX
XX 30-AUG-2001.
XX
XX 21-FEB-2001; 2001WO-US005896.
XX
XX 24-FEB-2000; 2000US-0185213P.
XX 16-MAY-2000; 2000US-0205232P.
XX 17-MAY-2000; 2000US-0205285P.
XX 17-MAY-2000; 2000US-0205286P.
XX 17-MAY-2000; 2000US-0205287P.
XX 17-MAY-2000; 2000US-0205323P.
XX 17-MAY-2000; 2000US-0205324P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX

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PI Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC,
PI Chen A, D'sa SA, Ameshey S, Dahl CR, Dam TC, Daniels SE, Dufour GB,
PI Flores V, Fong WT, Greenwalt IB, Hillman JL, Jones AL, Liu TF,
PI Roseberry AM, Rosen BH, Russo FD, Stockbrecher TK, Daffo A,
PI Wright RJ, Yap PS, Yu JY, Bradley DL, Bratcher SR, Chen W,
PI Cohen HU, Hodgson DM, Lincoln SE, Jackson S;
DR MPI; 2001-570631/64.
DR N-PSDB; AAS42521.
XX
XX
XX New disease detection and treatment molecule polynucleotides and
PT polypeptides, useful for diagnosis and treatment of arteriosclerosis,
PT cirrhosis, psoriasis, cancer, autoimmune disorders, diabetes mellitus,
PT asthma and multiple sclerosis.
PS
PS Claim 27; Page 180-182; 183pp; English.
XX
XX The invention relates to novel human molecules for disease detection and
CC treatment (mddt proteins) and the polynucleotides encoding them. The MDDT
CC polynucleotides and polypeptides are useful for diagnostic and
CC therapeutic purposes e.g. to diagnose and treat cell proliferative
CC disorders (e.g. arteriosclerosis, cirrhosis and psoriasis) cancers (e.g.
CC adenocarcinoma, leukemia and breast cancer) autoimmune disorders (e.g.
CC acquired immunodeficiency syndrome (AIDS) and Addison's disease) diabetes
CC mellitus, asthma, multiple sclerosis, osteoarthritis, and many more
CC diseases given in the specification. The present sequence represents an
CC mddt protein of the invention
XX
SQ Sequence 781 AA;
Query Match 96.8%; Score 4021; DB 4; Length 781;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTKDEPIVKSFFHVCMLIIIVGTRIOFSDGNEFAVDKSKRGLIHVPKDLPLKTKVLDMS 60
DB 7 MTKDEPIVKSFFHVCMLIIIVGTRIOFSDGNEFAVDKSKRGLIHVPKDLPLKTKVLDMS 66
QY 61 QNYIAELOVSDMSFISELTIVRLSHNRIOQLDLSVFKFNODLEYDLSHNOLOKISCHPI 120
DB 67 QNYIAELOVSDMSFISELTIVRLSHNRIOQLDLSVFKFNODLEYDLSHNOLOKISCHPI 126
QY 121 VSPRHLDSFNDKFLPTCKEFGNLSQNLFLGLSAMKLOKDLPLPAHHLSTYILDLRN 180
DB 127 VSPRHLDSFNDKFLPTCKEFGNLSQNLFLGLSAMKLOKDLPLPAHHLSTYILDLRN 186
QY 181 YYIKENETESLOILNAKTLHLVHFPTSLFAIQVNISVNTLGLQLOLTNIKANDNCQVFIK 240
DB 187 YYIKENETESLOILNAKTLHLVHFPTSLFAIQVNISVNTLGLQLOLTNIKANDNCQVFIK 246
QY 241 FLSELTIRSTLINFNLNHEETWKLIVRFQFLMKRPVAYLNIYNTTIESTREDFYYS 300
DB 247 FLSELTIRSTLINFNLNHEETWKLIVRFQFLMKRPVAYLNIYNTTIESTREDFYYS 306
QY 301 KTKLALTEHTHTNOVFLFSOTALATVFESENNIMMLTISDPFIHMLCPHASTFKPLNF 360
DB 307 KTKLALTEHTHTNOVFLFSOTALATVFESENNIMMLTISDPFIHMLCPHASTFKPLNF 366
QY 361 TQNVFTDSIFEKCSFLVLETLILQKNGIKDLFKVGLMTKMPSEIILDVSNNSLESGRH 420
DB 367 TQNVFTDSIFEKCSFLVLETLILQKNGIKDLFKVGLMTKMPSEIILDVSNNSLESGRH 426
QY 421 KENCWWSIIVNLNSSNMULTSVRCPLPRIKUTDHSNKKISPKQVYKLEALQELNV 480
DB 427 KENCWWSIIVNLNSSNMULTSVRCPLPRIKUTDHSNKKISPKQVYKLEALQELNV 486
QY 481 AFNSLTJDPGCGSFSSLSVLIIIDHNSVSHPSADFPQSCQKMSIKAGNDFPQCTELREF 540
DB 487 AFNSLTJDPGCGSFSSLSVLIIIDHNSVSHPSADFPQSCQKMSIKAGNDFPQCTELREF 546
QY 541 VKNIDQVSSEVLGMPDSYKCDYPPSYRSGSPDKDFHMSLSCNTLLIYTGATMLVLAV 600
DB 547 VKNIDQVSSEVLGMPDSYKCDYPPSYRSGSPDKDFHMSLSCNTLLIYTGATMLVLAV 606

QY 601 TWTSLCTIYDLPMYLRMVCOWTQTRRRANIPLEELQRLQPHAFISYSEHDSAMWKSSEL 660
DB 607 TWTSLCTIYDLPMYLRMVCOWTQTRRRANIPLEELQRLQPHAFISYSEHDSAMWKSSEL 666
QY 661 VPLEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSIFFVLSPNFVQSEWCHYELFYFAH 720
DB 667 VPLEKEDIQICLHERNFVPGKSIYENIINCIEKSYKSIFFVLSPNFVQSEWCHYELFYFAH 726
QY 721 HNLFFHGSNNLLILLLEPIQNSIPNKYHKLKALMTORTYLOMPKSKRG 771
DB 727 HNLFFHGSNNLLILLLEPIQNSIPNKYHKLKALMTORTYLOMPKSKRG 777
RESULT 11
ADU23197
ID ADU23197 standard; protein; 795 AA.
XX
XX ADU23197;
XX
XX 27-JAN-2005 (first entry)
XX
XX Murine Toll-like receptor 6 (TLR6) protein - SEQ ID 89.
XX
XX screening; Toll-like receptor agonist; TLR agonist; TLR6.
XX
XX Mus sp.
XX
XX WO2004094671-A2.
XX
XX 04-NOV-2004.
XX
XX 22-APR-2004; 2004WO-US012788.
XX
XX 22-APR-2003; 2003US-0464586P.
XX
XX 22-APR-2003; 2003US-0464588P.
XX
XX (COLE-) COLEY PHARM GMBH.
XX
XX (COLE-) COLEY PHARM GROUP INC.
XX
XX Volmer J, Jark M, Lidford GB, Schetter C, Forebach A, Krieg AM,
DR MPI; 2004-795573/78.
XX
XX Identifying agonists of Toll-like receptor (TLR) signaling activity,
XX useful therapeutically or prophylactically, comprises contacting an
XX PT RPM18226 cell that expresses a TLR with a test compound and measuring TLR
XX PT signaling activity.
XX
XX Disclosure; SEQ ID NO 89; 342pp; English.
XX
XX The invention comprises a screening method for identifying agonists of
XX CC Toll-like receptor (TLR) signaling activity. The method involves
XX CC contacting an RPM18226 cell (that expresses a TLR) with a test compound,
XX CC and measuring a test level of TLR signaling activity, where a test level
XX CC that is positive is indicative of a test compound that is a TLR agonist.
XX CC The method of the invention is useful for identifying agonists of TLR.
XX
XX The present amino acid sequence represents a TLR protein.
XX
SQ Sequence 795 AA;
Query Match 75.7%; Score 3144.5; DB 8; Length 795;
Best Local Similarity 73.9%; Pred. No. 3.9e-254;
Matches 588; Conservative 97; Mismatches 110; Indels 1; Gaps 1;
QY 1 MTKDEPIVKSFFHVCMLIIIVGTRIOFSDGNEFAVDKSKRGLIHVPKDLPLKTKVLDMS 60
DB 1 MSQDRKPIVGSFFHVCALALIVGWSMTSPSNELESWVDYNNRULTHVPKDLPERTKALISLS 60
QY 61 QNYIAELOVSDMSFISELTIVRLSHNRIOQLDLSVFKFNODLEYDLSHNOLOKISCHPI 120
DB 61 QNSISELMPIISFISELTIVRLSHNRIRISLDHFVFLFNODLEYDLSHNRLONTISCCPM 120

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QY 121 VSPRHLDISFNDPKALPICKEFGNLSQNLFLGLSAMKLOKLDLPIAHLSYILLDRN 180
Db 121 ASLHRLDISFNDPDLVPCKEFGNLTXTLTLPLGLSNAKFRQDLDPVAHLHLSCTILLDVS 180
QY 181 YYIKENETESIQLINAKTLHLVPHFTSLFAIQVINSVNTLGCLQTLNKKANDNCQVFIK 240
Db 181 YHIKGFETESIQLIPNTTVLHLVPHFNSLSFSQVQVNSVALGHLQLSNKKANDNCQRLMT 240
QY 241 FLSELTRGSLTLNPLNHLIETTWKCLVAVFOPLMKPPEYININYLITLIESIREDEFTYS 300
Db 241 FLSELTRGPTLLNLTLOHIEETWKCSVKLFQFPWRPPEYININYLITLTERIDREEFYIS 300
QY 301 KTTLKALTIETHTNOVFLFSQALYTVSENNIMMLTISDPFIHMLCPHAPSTFKPLNF 360
Db 301 ETALKSLMIEHVKNQVFLPSKALYSVFAEMNIKMLISDPFIHMCPPSPSFTPLNF 360
QY 361 TONVFTDSIFPKCSTLVKLETLILQKNGIKDLFKVGLMTKMPSLIILDVSNLSGRH 420
Db 361 TONVFTDSVFOGCSLTIKRLQTLILQKNGIKDFKVALMTKNSSLETILDVSNLSNSHAY 420
QY 421 KENCWVSEIIVNLSSNMLTDSVFRCLPPIKVLDLHSNKIKSVKQVVKLEALOELNV 480
Db 421 DRTCAMASILVNLSSNMLTSGVFRCLPPIKVLDLHNNRIMSIPKQVTHLOALOELNV 480
QY 481 AFNSLTLDIPGCGSFSSLSVLIIDHNSVSHPSADPFQSCQKMSIRAGDNPFQCTCELBEF 540
Db 481 ASNSLTLDIPGCGAFSSLSVLIIDHNSVSHPSADPFQSCQKMSIRAGDNPFQCTCELBEF 540
QY 541 VKNIDQVSSEVLGMPDSYKCDYPESYRGSPLKDFHMSBLSCNITLLIYTTGATMLVLAV 600
Db 541 VKNIGWVAREVEGMPDSYKCDYPESYRGSPLKDFHMSBLSCNITLLIYTTGATMLVLAV 600
QY 601 TWTSLCTIYLDLPWYLRMVCOWTQTRRARNTPLEELQRLQPHAFISYSEHDSAWKSEL 660
Db 601 TGAFLCTIYFDLPWYLRMVCOWTQTRRARNTPLEELQRLQPHAFISYSEHDSAWKSEL 660
QY 661 VPELEKEDIQICLHERNFYPGKSIYENINICIEKSYKSIYVLSPNFVQSEWCHYELYPFH 720
Db 661 LPLNEKEDIRVCLHERNFYPGKSIYENINIFIEKSKAIFVLSPHIQSEWCHYELYPFH 720
QY 721 HNLFHSGSNLLILILEPIPNISIPNKYHKLKALMTQRTYLOMPKESKRGFLMANIRPA 780
Db 721 HNLFHSGSNLLILILEPIPNISIPNKYHKLKALMTQRTYLOMPKESKRGFLMANIRPA 780
QY 781 FNMKLTLYTENNDDYKS 796
Db 781 FNMKLTLYTENNDDYKS 796
Db 781 FTMKLTLYNE-DDVKT 795

RESULT 12
ADU23195
ID ADU23195 standard; protein; 806 AA.
XX
AC ADU23195;
XX
XX 27-JAN-2005 (first entry)
XX
XX Murine Toll-like receptor 6 (TLR6) protein - SEQ ID 87.
XX
XX screening; Toll-like receptor agonist; TLR agonist; TLR6.
XX
XX Mus sp.
XX
XX WO2004094671-A2.
XX
XX 04-NOV-2004.
XX
XX 22-APR-2004; 2004MO-US012788.
XX
XX 22-APR-2003; 2003US-0464586P.
XX
XX 22-APR-2003; 2003US-0464588P.
XX
XX (COLE-) COLEY PHARM GMBH.

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PA (COLE-) COLEY PHARM GROUP INC.
XX
XX Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
XX WPI; 2004-795573/78.
XX
XX Identifying agonists of Toll-like receptor (TLR) signaling activity,
XX useful therapeutically or prophylactically, comprises contacting an
XX PT RPM18226 cell that expresses a TLR with a test compound and measuring TLR
XX signaling activity.
XX
XX Disclosure; SEQ ID NO 87; 342bp; English.
XX
XX The invention comprises a screening method for identifying agonists of
XX CC Toll-like receptor (TLR) signaling activity. The method involves
XX CC contacting an RPM18226 cell (that expresses a TLR) with a test compound,
XX CC and measuring a test level of TLR signalling activity, where a test level
XX CC that is positive is indicative of a test compound that is a TLR agonist.
XX CC The method of the invention is useful for identifying agonists of TLR.
XX CC The present amino acid sequence represents a TLR protein.
XX
XX Sequence 806 AA;
SQ
Query Match 75.7%; Score 3144.5; DB 8; Length 806;
Best Local Similarity 72.9%; Pred. No. 4e-254;
Matches 588; Conservative 97; Mismatches 110; Indels 1; Gaps 1;
QY 1 MTKDKETIVKSFHFVCLMIIIVGTIRIOFSDGNEFVADSKRKLTHVPKDLPLKTKVLDMS 60
Db 12 MSQDRKPIVGSFHVYCALALVSGMTFRSNLEGMVYSNNNLHVPKDPAPRRKALSLIS 71
QY 61 QNYIAELQVSDMSFLSELTVLRLSHNRILQILDLSVFKENODLEYILDVSHNOLOKISCHPI 120
Db 72 QNSISELMPDISFELSELVLRILSHNRIRSDPFVFLFNODLEYILDVSHNLOMISCCPM 131
QY 121 VSPRHLDISFNDPKALPICKEFGNLSQNLFLGLSAMKLOKLDLPIAHLSYILLDRN 180
Db 121 ASLHRLDISFNDPDLVPCKEFGNLTXTLTLPLGLSNAKFRQDLDPVAHLHLSCTILLDVS 191
QY 181 YYIKENETESIQLINAKTLHLVPHFTSLFAIQVINSVNTLGCLQTLNKKANDNCQVFIK 240
Db 181 YHIKGFETESIQLIPNTTVLHLVPHFNSLSFSQVQVNSVALGHLQLSNKKANDNCQRLMT 251
QY 241 FLSELTRGSLTLNPLNHLIETTWKCLVAVFOPLMKPPEYININYLITLIESIREDEFTYS 300
Db 241 FLSELTRGPTLLNLTLOHIEETWKCSVKLFQFPWRPPEYININYLITLTERIDREEFYIS 311
QY 301 KTTLKALTIETHTNOVFLFSQALYTVSENNIMMLTISDPFIHMLCPHAPSTFKPLNF 360
Db 312 ETALKSLMIEHVKNQVFLPSKALYSVFAEMNIKMLISDPFIHMCPPSPSFTPLNF 371
QY 361 TONVFTDSIFPKCSTLVKLETLILQKNGIKDLFKVGLMTKMPSLIILDVSNLSGRH 420
Db 372 TONVFTDSVFOGCSLTIKRLQTLILQKNGIKDFKVALMTKNSSLETILDVSNLSNSHAY 431
QY 421 KENCWVSEIIVNLSSNMLTDSVFRCLPPIKVLDLHSNKIKSVKQVVKLEALOELNV 480
Db 432 DRTCAMASILVNLSSNMLTSGVFRCLPPIKVLDLHNNRIMSIPKQVTHLOALOELNV 491
QY 481 AFNSLTLDIPGCGSFSSLSVLIIDHNSVSHPSADPFQSCQKMSIRAGDNPFQCTCELBEF 540
Db 492 ASNSLTLDIPGCGAFSSLSVLIIDHNSVSHPSADPFQSCQKMSIRAGDNPFQCTCELBEF 551
QY 541 VKNIDQVSSEVLGMPDSYKCDYPESYRGSPLKDFHMSBLSCNITLLIYTTGATMLVLAV 600
Db 552 VKNIGWVAREVEGMPDSYKCDYPESYRGSPLKDFHMSBLSCNITLLIYTTGATMLVLAV 611
QY 601 TWTSLCTIYLDLPWYLRMVCOWTQTRRARNTPLEELQRLQPHAFISYSEHDSAWKSEL 660
Db 612 TGAFLCTIYFDLPWYLRMVCOWTQTRRARNTPLEELQRLQPHAFISYSEHDSAWKSEL 671
QY 661 VPELEKEDIQICLHERNFYPGKSIYENINICIEKSYKSIYVLSPNFVQSEWCHYELYPFH 720
Db 661 VPELEKEDIQICLHERNFYPGKSIYENINICIEKSYKSIYVLSPNFVQSEWCHYELYPFH 720

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Db      672 LPELEKDIRVCLHERNFVPGKSIYENINIFLEKSYKALFVLSPHFIOSEWCHYELEYFAH 731
Qy      721 HNLPHFGSNNLILILEPIPNKHYHKLKALMTORTYLOMPKESKRGLFMANIRAA 780
Db      732 HNLPHFGSNNLILILEPIPNKHYHKLKALMTORTYLOMPKESKRGLFMANIRAS 791
Qy      781 FNMKLTLYTENNDVKS 796
Db      792 FIMKTLALVNE-DVKT 806

RESULT 13
ID      AAY8055
AA      AAY8055 standard; protein; 806 AA.
AC      AAY8055;
XX
XX      22-SEP-2000 (first entry)
XX
XX      Murine Toll-like receptor TLR6 protein.
XX
XX      Toll-like receptor; TLR6; murine; anti-infectious; treatment; infection;
XX      transcription factor; NF-kappaB; immune response.
XX      Mus sp.
XX      WO200024776-A1.
XX      04-MAY-2000.
XX      26-OCT-1999; 99WO-JP005917.
XX      26-OCT-1998; 98JP-00304110.
XX      26-OCT-1998; 98JP-00304110.
XX      (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX      Akira S, Takeuchi O;
XX      WPI: 2000-350697/30.
XX      N-PSDB; AAA39810.
XX      Toll-like receptor TLR6 molecule and encoded gene, participating in
XX      signal transduction of initial immune response, applicable e.g. in
XX      treating infections.
XX
XX      Claim 1; Page 31-33; 35pp; Japanese.
XX
XX      This invention describes a novel toll-like receptor TLR6 which has
XX      anti-infectious activity. The protein and its encoded gene have clinical
XX      use e.g. in treating infections. Toll family receptors are related to
XX      transcription factor NF-kappaB and regulate the expression of various
XX      genes participating in the immune response. This sequence represents the
XX      murine TLR6 protein which is described in the method of the invention
XX
XX      Sequence 806 AA;

Query Match      75.6%; Score 3139.5; DB 3; Length 806;
Best Local Similarity 73.7%; Pred. No. 1e-253;
Matches 587; Conservative 98; Mismatches 110; Indels 1; Gaps 1;

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Db      192 HHKGGFETESLQIPNTVYLHLVFNHNSLFSVQVNNNSVALGHLQSLNKINDENCORLMT 251
Qy      241 FLSLETRGSLTNLNFNLHETTKCLVRFQFLMKPEYELINYULTTIESREDFTYS 300
Db      252 FLSLETRGSLTNLNFNLHETTKCLVRFQFLMKPEYELINYULTTIESREDFTYS 311
Qy      301 KTLKALTEHTNTQVPLFSOTALTVESENNIMULTSDPEFIMLCPHASTKFLNF 360
Db      312 ETALKSLMEIHEVKQVFLFSKALYSVFAENNIKMLISIDTFFIMVDCPSSSSTFLNF 371
Qy      361 TQNVFTDSIFKCSSTLVKLETLILQKNGKDLFKVGLMTKMPSEIIDVSNNSSESGRH 420
Db      372 TQNVFTDSVFGCCSTLXKLQTLILQKNGKDLFKVGLMTKMPSEIIDVSNNSSESGRH 431
Qy      421 KENCTWVESIVVNLNLSNNMLTDSVRCCLPRKIVLDHNSKTKSVPKOVYKLEALQELNV 480
Db      432 DRTCAMAESILVNLNLSNNMLTDSVRCCLPRKIVLDHNSKTKSVPKOVYKLEALQELNV 491
Qy      481 AFNSLITDLPGCGSPSSLSVLIIIDHNSVSHPSADFPQSCQKMSIKAGDNPCCTELREF 540
Db      492 ASNSLITDLPGCGSPSSLSVLIIIDHNSVSHPSADFPQSCQKMSIKAGDNPCCTELREF 551
Qy      541 VKNIDQVSEVLEGPDPDSYKCDPESYRGSPLKDFHMSLSCNITLITVIGATMLVLAV 600
Db      552 VKNIGVAREVEVEGPDSDYKCDPESYRGSPLKDFHMSLSCNITLITVIGATMLVLAV 611
Qy      601 TVTSLCTIYLDLPWYLRWVQWOTRRARNIPLEELQNLQGHAFISYSEHDSAVKSEL 660
Db      612 TGAFLCTLYFDLPWYLRWVQWOTRRARNIPLEELQNLQGHAFISYSEHDSAVKSEL 671
Qy      661 VPLEKEDIOICLHERNFVPGKSIYENININCEKYSKIFVLSPHFIOSEWCHYELEYFAH 720
Db      672 LPELEKDIRVCLHERNFVPGKSIYENININCEKYSKIFVLSPHFIOSEWCHYELEYFAH 731
Qy      721 HNLPHFGSNNLILILEPIPNKHYHKLKALMTORTYLOMPKESKRGLFMANIRAA 780
Db      732 HNLPHFGSNNLILILEPIPNKHYHKLKALMTORTYLOMPKESKRGLFMANIRAS 791
Qy      781 FNMKLTLYTENNDVKS 796
Db      792 FIMKTLALVNE-DVKT 806

RESULT 14
ID      ADU23194
AA      ADU23194 standard; protein; 806 AA.
AC      ADU23194;
XX
XX      27-JAN-2005 (first entry)
XX
XX      Murine Toll-like receptor 6 (TLR6) protein - SEQ ID 86.
XX
XX      screening; Toll-like receptor agonist; TLR agonist; TLR6.
XX
XX      Mus sp.
XX      WO2004094671-A2.
XX      04-NOV-2004.
XX      22-APR-2004; 2004WO-US012788.
XX      22-APR-2003; 2003US-0464586P.
XX      22-APR-2003; 2003US-0464586P.
XX      (COLE-) COLEY PHARM GMBH.
XX      (COLE-) COLEY PHARM GROUP INC.
XX      Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
XX      WPI: 2004-795573/78.

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QY 241 FISELTRGSLINFTLNHIETTMKCLAVFOELMPKVEYININYLTIIIESIREEDFTYS 300
 DB 253 FISELTRGPTLNVLTQHIEITTMKCSVKLFQFFWPRPVEYININYLTIERIDREBFTYS 311
 QY 301 KTTLKALTEHTNOVFLFSQALYTVFSEKMINIMLTISDTPFIHMLCPHADSTFKELNF 360
 DB 312 ETALKSIMIEHYKNOVFLFSKALYSVFAPENMIKMLISIDTPFIHMCPPSPSSFTFLNF 371
 QY 361 TONVFTDSIFEKCSLTVKLETLILQKNGKDLFKVGLMTKDMPSLEILDVSNWSLESGRH 420
 DB 372 TONVFTDSVFGQSTLKRLOTLILQKNGKDNFVKALMTKNMSSLETLDVSNWSINSINSHAY 431
 QY 421 KENCTVRESIVVNLNSSNMLTDSVFRCLPPRIKVIDLHNSNKIKSVPOVVKLEALQELNV 480
 DB 432 DRTCAMABESILVNLNSSNMLTGSVFRCLPPKAVLDLHNNRIMSTPKDYTHLOALQELNV 491
 QY 481 AFNSLTDLPGCGSFSSLSVLIIDHNSVSHPSADFFQSCQKMSIKAGDNPFOCTCELREF 540
 DB 492 ASNSLTDLPGCGAFSSLSVLIIDHNSVSHPSDEDFQSCQNIIRSLTAGNNPFOCTCELREF 551
 QY 541 VKNIDQVSESEVLEGWDSYKCDYPESYRGSPLKDFHMSLSCTITLITVIGATMLVLAV 600
 DB 552 VKNIGVAREVEGWDPDSYRCDYPESKGTALRDFHMSPLSCDTVLLTVTIGATMLVLAV 611
 QY 601 TVTSLCIYDLPMYLRMVCOMTQTRRRANIPLEELQRMLOFHAFISYSEHDSAWYKSEL 660
 DB 612 TGAFLCIFYDLPMYLRMVCOMTQTRRRANIPLEELQRMLOFHAFISYSEHDSAWYKSEL 671
 QY 661 VPELEKEDIQICLHERNFVPGKSIVENIINICIEKSYKSI FVLSPNFVQSEWCHYELYPFH 720
 DB 672 LFNLEKDDIRVCLHERNFVPGKSIVENIINFIEKSYKALFVLSPHFIQSEWCHYELYPFH 731
 QY 721 HNLFFHGSNNLILILIEPIPNKIKYKALKALMTQRTYLOPKKSKRGLEFWANIRAA 780
 DB 732 HNLFFHGSNNLILILIEPIPNKIKYKALKALMTQRTYLOPKKSKRGLEFWANIRAS 791
 QY 781 FNMKLLTVTENNDVKS 796
 DB 792 FIMKLLLVNE-DDVKT 806

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 Job time : 114 secs

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XX The invention relates to a novel expression system comprising a first
CC nucleic acid sequence that encodes a Toll-like receptor (TLR) operably
CC linked to a first expression control sequence and a second nucleic acid
CC sequence that encodes a reporter. TLRs are immune response modifiers
CC (IRMs). The expression system of the invention may be useful for
CC preparing a composition comprising the TLR agonist for treating cancer,
CC possibly via gene therapy. The current sequence is that of the human Toll
CC -like receptor TLR6 DNA (SEQ ID 11) of the invention.
XX

Sequence 2753 BP; 849 A; 559 C; 507 G; 838 T; 0 U; 0 Other;

Query Match 100.0%; Score 2753; DB 12; Length 2753;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGAATTGGACCTCATATCAGATGCTCTGGAAGAAGCAACCTTAGATGCCACCTGC 60
DB 1 AGAATTGGACCTCATATCAGATGCTCTGGAAGAAGCAACCTTAGATGCCACCTGC 60
QY 61 AACATCATGACCAAGACCAAGAACCTATTGTTAAAAGCTTCCATTGTTGCCCTTAAG 120
DB 61 AACATCATGACCAAGACCAAGAACCTATTGTTAAAAGCTTCCATTGTTGCCCTTAAG 120
QY 121 ATCATTAATAGTTGGAACCAAGATCCAGATCTCCGACGGAATGAATTTGSCAGTAGACAAG 180
DB 121 ATCATTAATAGTTGGAACCAAGATCCAGATCTCCGACGGAATGAATTTGSCAGTAGACAAG 180
QY 181 TCAAAAAGAGCTTATTCATTCATTCCTCAAAAAGACCTACCGCTGAAAAACCAAACTCTTAAGT 240
DB 181 TCAAAAAGAGCTTATTCATTCATTCCTCAAAAAGACCTACCGCTGAAAAACCAAACTCTTAAGT 240
QY 241 ATGTCTCAAGAACTACATCGCTAGCTTCAAGTCTCTGACATGAGCTTTCTACAGAGTTG 300
DB 241 ATGTCTCAAGAACTACATCGCTAGCTTCAAGTCTCTGACATGAGCTTTCTACAGAGTTG 300
QY 301 ACAGTTTGGAGACTTTCCTCCATAACAGAAATCCAGCTACTGATTAAAGTCTTCAAGTTC 360
DB 301 ACAGTTTGGAGACTTTCCTCCATAACAGAAATCCAGCTACTGATTAAAGTCTTCAAGTTC 360
QY 361 AACCGAGATTGAGATTTGATTTGATTTATCTCATTAATCACTTGGCAAAAAGATATCTGGCCAT 420
DB 361 AACCGAGATTGAGATTTGATTTGATTTATCTCATTAATCACTTGGCAAAAAGATATCTGGCCAT 420
QY 421 CCTATTGGAGTTGAGGCAATTAGATCTCTCATTCATGATTTTCAAGGCCCTGCCCATC 480
DB 421 CCTATTGGAGTTGAGGCAATTAGATCTCTCATTCATGATTTTCAAGGCCCTGCCCATC 480
QY 481 TGTAAAGAAATTTGGCACTTATCAACAAGTGAATTTCTTGGAGTTGAGTGTCTATGAAGCTG 540
DB 481 TGTAAAGAAATTTGGCACTTATCAACAAGTGAATTTCTTGGAGTTGAGTGTCTATGAAGCTG 540
QY 541 CAAAAATTAGATTGCTGCAATGTCTCACTTGCACTTAAGTTATCTCTTGAGTTTA 600
DB 541 CAAAAATTAGATTGCTGCAATGTCTCACTTGCACTTAAGTTATCTCTTGAGTTTA 600
QY 601 AGAATTTATATATATAAAGAAATGAGACAGAAAGTCTCAAAATTTCTGAATGCAAAAAC 660
DB 601 AGAATTTATATATATAAAGAAATGAGACAGAAAGTCTCAAAATTTCTGAATGCAAAAAC 660
QY 661 CTTCACCTTGTGTTTTCACCCAACTAGTTTATTCGCTATCCAAAGTGAACATATCAGTTAAT 720
DB 661 CTTCACCTTGTGTTTTCACCCAACTAGTTTATTCGCTATCCAAAGTGAACATATCAGTTAAT 720
QY 721 ACTTAGAGGTGCTTACAACTGACTAATATTAATGAATGACAACTGCAAGTTTC 780
DB 721 ACTTAGAGGTGCTTACAACTGACTAATATTAATGAATGACAACTGCAAGTTTC 780
QY 781 ATTAATTTTATTCAGAACTCAACAGAGGTTCAACTTCTGATGATTTTCACTCAACAC 840
DB 781 ATTAATTTTATTCAGAACTCAACAGAGGTTCAACTTCTGATGATTTTCACTCAACAC 840
QY 841 ATAGAAGCACTTGAATGCTGCTGATCAGAGTCTTTCAAATTTCTTGGCCCAAACTGTG 900
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DB 841 ATAGAAGCACTTGAATGCTGCTGATCAGAGTCTTTCAAATTTCTTGGCCCAAACTGTG 900
QY 901 GAATATCTCAATATTTATTAACAATTTAAACAATATTTGAAGCATTCGGAAGATTTTACT 960
DB 901 GAATATCTCAATATTTATTAACAATTTAAACAATATTTGAAGCATTCGGAAGATTTTACT 960
QY 961 TATTTGAAACGACATTTGAAAGCATTTGACAAATGAAACATATTCAGAACCAAGTTTCTG 1020
DB 961 TATTTGAAACGACATTTGAAAGCATTTGACAAATGAAACATATTCAGAACCAAGTTTCTG 1020
QY 1021 TTTTACAGACAGCTTTGTACACCGTGTGTTTCTGAGATGAACATTAATGTAACCAT 1080
DB 1021 TTTTACAGACAGCTTTGTACACCGTGTGTTTCTGAGATGAACATTAATGTAACCAT 1080
QY 1081 TCAGATACACCTTTTATACATGCTGTGCTCCTCAGCACCAGACCAATTCAGTTTCTG 1140
DB 1081 TCAGATACACCTTTTATACATGCTGTGCTCCTCAGCACCAGACCAATTCAGTTTCTG 1140
QY 1141 AACTTTACCCAGAAAGCTTTTACAGATAGTATTTTGAAGAAATGTTCCACGTTAGTTAAA 1200
DB 1141 AACTTTACCCAGAAAGCTTTTACAGATAGTATTTTGAAGAAATGTTCCACGTTAGTTAAA 1200
QY 1201 TTGAGACACTTATCTTCAAAAAATGATTAAGACCTTTTCAAGTAGTCTCATG 1260
DB 1201 TTGAGACACTTATCTTCAAAAAATGATTAAGACCTTTTCAAGTAGTCTCATG 1260
QY 1261 ACGAAGATATGCTCTTCTTGGAAATATCTGATGTTAGCTGGAATCTTGGAAATCTGCT 1320
DB 1261 ACGAAGATATGCTCTTCTTGGAAATATCTGATGTTAGCTGGAATCTTGGAAATCTGCT 1320
QY 1321 AGACATTAAGAAACCTGACCTTGGTGAAGATATAGTGTGTTAAATTTGTCTTCAAT 1380
DB 1321 AGACATTAAGAAACCTGACCTTGGTGAAGATATAGTGTGTTAAATTTGTCTTCAAT 1380
QY 1381 ATGCTTACTGACTCTGTTTTCAGATGTTTACCCTCCAGATCAAGTACTTGAATCTTAC 1440
DB 1381 ATGCTTACTGACTCTGTTTTCAGATGTTTACCCTCCAGATCAAGTACTTGAATCTTAC 1440
QY 1441 AGCAATTAATAATTAAGAGGCTTCTTAACAAGTCGTAACAGTCTTTCGAAAGATCTG 1500
DB 1441 AGCAATTAATAATTAAGAGGCTTCTTAACAAGTCTTTCGAAAGATCTG 1500
QY 1501 AATGTTGCTTTCATTTCTTAACTGACCTTCTGAGTGGCAAGCTTTAGACGCTTTCT 1560
DB 1501 AATGTTGCTTTCATTTCTTAACTGACCTTCTGAGTGGCAAGCTTTAGACGCTTTCT 1560
QY 1561 GTATTGATCATTTGATCACAATTTCAAGTTTCCACCAATGGCTGATTTCTTCCAGAGCTGC 1620
DB 1561 GTATTGATCATTTGATCACAATTTCAAGTTTCCACCAATGGCTGATTTCTTCCAGAGCTGC 1620
QY 1621 CAGAGATGAGGTCAATTAAGCAGGGAGCAATTCATTCGAATGTACCTGTGAGTAAAGA 1680
DB 1621 CAGAGATGAGGTCAATTAAGCAGGGAGCAATTCATTCGAATGTACCTGTGAGTAAAGA 1680
QY 1681 GAATTTGTCAAAAAATATAGACCAAGTATCAAGTGAAGTGTAGAGGGCTGGCTGATTTCT 1740
DB 1681 GAATTTGTCAAAAAATATATAGACCAAGTATCAAGTGAAGTGTAGAGGGCTGGCTGATTTCT 1740
QY 1741 TATTAAGTGTGACTACCCGAAAAGTTATAGAGAAAGCCCACTTAAGAGCTTTTCACTGTCT 1800
DB 1741 TATTAAGTGTGACTACCCGAAAAGTTATAGAGAAAGCCCACTTAAGAGCTTTTCACTGTCT 1800
QY 1801 GAAATATCTGCAACATAACTCTGTGATTCGTCACATCTGGTGCCACCATGCTGGTGTG 1860
DB 1801 GAAATATCTGCAACATAACTCTGTGATTCGTCACATCTGGTGCCACCATGCTGGTGTG 1860
QY 1861 GCTGTGACTGTGACCTCCCTCTGCACTTACTGATGATCTGCTGTGATCTCAGATGTG 1920
DB 1861 GCTGTGACTGTGACCTCCCTCTGCACTTACTGATGATCTGCTGTGATCTCAGATGTG 1920
QY 1921 TGCAGTGGACCCAGACTCGGGCGAGGGCCAGGAACATACCTTTGAAGAACTCCAAAGA 1980
DB 1921 TGCAGTGGACCCAGACTCGGGCGAGGGCCAGGAACATACCTTTGAAGAACTCCAAAGA 1980
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Db	1921	GGCCAGTGGAGCCACAGACTGGGGGCGAGGGGCAAGAACTAACCCCTTAGAAGAACTCCAAAGA	1980
OY	1981	AACCTCCAGTTTCACTGCTTTTATTTTCATATAGTGAACATGATTTCTGCTGGGTGAAAAGT	2040
Db	1981	AACCTCCAGTTTCACTGCTTTTATTTTCATATAGTGAACATGATTTCTGCTGGGTGAAAAGT	2040
OY	2041	GAATTGTATCCTTACTTGAAGAAAAAGATATACGATTTTGTCTTCATGAAGAACCTTT	2100
Db	2041	GAATTGTATCCTTACTTGAAGAAAAAGATATACGATTTTGTCTTCATGAAGAACCTTT	2100
OY	2101	GTCCCTGGCAAGAGACTGTGGAAAAATATCATCACTGCATTTGAGAAAGATTAACAAGTCC	2160
Db	2101	GTCCCTGGCAAGAGACTGTGGAAAAATATCATCACTGCATTTGAGAAAGATTAACAAGTCC	2160
OY	2161	ATCTTTGTTTTGTCTCCCAACTTTTGTCCAGAGTGAAGTGGTGCATTAAGAACTCTATTTT	2220
Db	2161	ATCTTTGTTTTGTCTCTCCCACTTTTGTCCAGAGTGAAGTGGTGCATTAAGAACTCTATTTT	2220
OY	2221	GCCCATCACAATCTCTTTTCATGAAAGATCTATATACTTAATCTCATCTTACTGGAAACC	2280
Db	2221	GCCCATCACAATCTCTTTTCATGAAAGATCTATATACTTAATCTCATCTTACTGGAAACC	2280
OY	2281	ATTCACACAAACAGCATTTCCCAACAGTACCAACAAGCTGAAGGCTCTCATGACGACGGG	2340
Db	2281	ATTCACACAGAAACAGCATTTCCCAACAGTACCAACAAGCTGAAGGCTCTCATGACGACGGG	2340
OY	2341	ACTTATTTGGCAGTGGCCCAAGAGAAAAAGCAAACTGGGCTCTTTTGGGCTMAACATTAGA	2400
Db	2341	ACTTATTTGGCAGTGGCCCAAGAGAAAAAGCAAACTGGGCTCTTTTGGGCTMAACATTAGA	2400
OY	2401	GCCGCTTTTATATGAAGAAATTAACTATGCACTGAAAACATMGATGTAATCTTAAAAA	2460
Db	2401	GCCGCTTTTATATGAAGAAATTAACTATGCACTGAAAACATMGATGTAATCTTAAAAA	2460
OY	2461	AATTTAGGAAATTCACCTTAAGAAACCATTAATTTACTTGGATGATGGAATGATGACAGT	2520
Db	2461	AATTTAGGAAATTCACCTTAAGAAACCATTAATTTACTTGGATGATGGAATGATGACAGT	2520
OY	2521	CGTAAAGTACTGTCTGAGGTGCTCCATTAATCTCATGACCTTCAGGAAAGACTTAAACA	2580
Db	2521	CGTAAAGTACTGTCTGAGGTGCTCCATTAATCTCATGACCTTCAGGAAAGACTTAAACA	2580
OY	2581	AAACCAATTTTCATCTGGGAACTGAGCTAGAGCGGTGAGTTAGCTGCCAGTTAGAGAC	2640
Db	2581	AAACCAATTTTCATCTGGGAACTGAGCTAGAGCGGTGAGTTAGCTGCCAGTTAGAGAC	2640
OY	2641	AGCCCAAGTCTCTTGGTTTATCATTAATGTTTCAMATGGAACAGTCTCTTTGAGATAA	2700
Db	2641	AGCCCAAGTCTCTTGGTTTATCATTAATGTTTCAMATGGAACAGTCTCTTTGAGATAA	2700
OY	2701	ATGCTCAATTTTCAAGCTCCTCCACCTGCTCTTCCCAATGGAATCTGTGG	2763
Db	2701	ATGCTCAATTTTCAAGCTCCTCTCCACTGCTCTTCCCAATGGAATCTGTGG	2763

RESULT 2	
ADP48600	
ID	ADP48600 standard; cDNA; 2753 BP.
XX	
AC	
XX	ADP48600;
DT	09-SEP-2004 (first entry)
XX	
DE	
XX	Human Toll-like receptor 6 encoding cDNA SEQ ID NO:11.
KW	Toll-like receptor; TLR; human; detection; identification; TLR agonist; TLR antagonist; Toll like receptor 6; TR6; chromosome 4; gene; ss.
OS	Homo sapiens.
FT	
CDS	Location/Qualifiers 67..2457 /*tag= a

FT	XX	/product= "Toll-like receptor 6"
FN	XX	
PD	XX	WO2004053452-A2.
PP	XX	24-JUN-2004.
PX	XX	
PR	XX	31-OCT-2003; 2003WO-US034554.
PS	XX	
PT	XX	11-DEC-2002; 2002US-0432650P.
RD	XX	(MINN) 3M INNOVATIVE PROPERTIES CO.
RP	XX	Gupta SK, Ghosh TK, Fink JR;
RQ	XX	WPI; 2004-468955/44.
SQ	XX	P-PDSB; ADP48601.
TG	XX	GENBANK; NM_006068.
TS	XX	Detecting activation of Toll-like receptors (TLR) for identifying a TLR
TT	XX	agonist or antagonist, comprises providing a cell culture comprising
TX	XX	cells transfected with a sequence encoding a reporter.
TY	XX	Claim 7; SEQ ID NO 11; 78bp; English.
ZZ	XX	The present invention describes a method for detecting activation of a
	XX	Toll-like receptor (TLR) in a cell. The method comprises: (a) providing a
	XX	cell culture comprising cells transfected with a nucleic acid sequence
	XX	that encodes a reporter that (i) generates a detectable signal when the
	XX	reporter is expressed and the cell is exposed to conditions for
	XX	generating the detectable signal, and (ii) is operably linked to an
	XX	expression control sequence that is induced by activation of a TLR and
	XX	comprises a cytokine promoter, a chemokine promoter, a co-stimulatory
	XX	marker promoter, or a defensin promoter; (b) exposing the cell culture to
	XX	a compound that activates a TLR; (c) providing conditions for generating
	XX	the detectable signal; and (d) detecting the detectable signal. Also
	XX	described: (1) a method of identifying a TLR agonist or antagonist; (2) a
	XX	TLR agonist or antagonist identified by the method of (1); and (3) a
	XX	pharmaceutical composition comprising a TLR agonist or antagonist
	XX	identified by the method of (1) and a pharmaceutical salt. The methods
	XX	are useful for detecting activation of a TLR in a cell and for
	XX	identifying TLR agonist or antagonist. The present sequence encodes a
	XX	human TLR6 which is used in the exemplification of the present invention.
	XX	The human TLR6 gene is located on chromosome 4, more specifically to
	XX	4p14.
SQ	Sequence 2753 BP; 849 A; 559 C; 507 G; 838 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 2753; DB 12; Length 2753;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 2753; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 AGAATTTGGACTCATATTCGAAGTGCTCGAAGAAACAACCCCTTAGATTGCCATCGC 60	
Db	1 AGAATTTGGACTCATATTCGAAGTGCTCGAAGAAACAACCCCTTAGATTGCCATCGC 60	
OY	61 AACATCATGCACCAAGAACAAGAACCTATTGTATAAAGCTTCCATTTGGTTGGCCTTAATG 120	
Db	61 AACATCATGCACCAAGAACAAGAACCTATTGTATAAAGCTTCCATTTGGTTGGCCTTAATG 120	
OY	121 ATCATTAATAGTTGGAACCAGAAATCCAGTTCTCCGACGGAATGAATTTGCAGTAGACAAG 180	
Db	121 ATCATTAATAGTTGGAACCAGAAATCCAGTTCTCCGACGGAATGAATTTGCAGTAGACAAG 180	
OY	181 TCAGAAAAGAGCTTATTCATGTTCCAAABAACCTAACCGGCGAAACCAAAGCTTTAGAT 240	
Db	181 TCAGAAAAGAGCTTATTCATGTTCCAAABAACCTAACCGGCGAAACCAAAGCTTTAGAT 240	
OY	241 ATGTCTCAGAACTACATCGCTGAGCTTCAGCTCTGACATGAGCTTCTATCAGAGTTG 300	
Db	241 ATGTCTCAGAACTACATCGCTGAGCTTCAGCTCTGACATGAGCTTCTATCAGAGTTG 300	
OY	301 ACAAGTTTGAACCTTTCCCATTAACGAATCCAGACTACTTGAATTTAGTGTTCAGATTTC 360	
Db	301 ACAAGTTTGAACCTTTCCCATTAACGAATCCAGACTACTTGAATTTAGTGTTCAGATTTC 360	

Db 301 ACAGTTTGAGACTTTCCCAATACAGAACTCAGCTTGTAAAGTGTTCAGAGTTC 360
Qy 361 AACCGAGATTGAAATATTTGGATTATCTCATTAATCAGTTGCGAAAGATATCTCGCAT 420
Db 361 AACCGAGATTGAAATATTTGGATTATCTCATTAATCAGTTGCGAAAGATATCTCGCAT 420
Qy 421 CCTATTTGAGTTTCAGGCATTTAAGTCTCTCATTCATGATGATTTCCAGGCCCTGCCATC 480
Db 421 CCTATTTGAGTTTCAGGCATTTAAGTCTCTCATTCATGATGATTTCCAGGCCCTGCCATC 480
Qy 481 TGTAGGAATTTGGCACTTATCACACAGATTTCTGGGAGTAGAGTCTATGAAGCTG 540
Db 481 TGTAGGAATTTGGCACTTATCACACAGATTTCTGGGAGTAGAGTCTATGAAGCTG 540
Qy 541 CAAAAATTAGATTCTGCGCAATTGCTCACTTGACCTTAAGTTAATCTCTTGAGATTTA 600
Db 541 CAAAAATTAGATTCTGCGCAATTGCTCACTTGACCTTAAGTTAATCTCTTGAGATTTA 600
Qy 601 AGAAATTTATATATATAAAGAAAATGAGACAGAAAGTCTACAAATTTCTGAATGCAAAAC 660
Db 601 AGAAATTTATATATATAAAGAAAATGAGACAGAAAGTCTACAAATTTCTGAATGCAAAAC 660
Qy 661 CTTCACCTGTTTTTCAACCACTGATTTATTCGCTATCCAGTGAACATACAGTTAT 720
Db 661 CTTCACCTGTTTTTCAACCACTGATTTATTCGCTATCCAGTGAACATACAGTTAT 720
Qy 721 ACTTTAGGGTGCTTACAACTGACTATAATTAATGAATGATGACAACTGTCAAGTTTC 780
Db 721 ACTTTAGGGTGCTTACAACTGACTATAATTAATGAATGATGACAACTGTCAAGTTTC 780
Qy 781 ATTTAATTTTATTCAGAACTCACAGAGGTTCAACCTTATGTAATTTTACCTCAACAC 840
Db 781 ATTTAATTTTATTCAGAACTCACAGAGGTTCAACCTTATGTAATTTTACCTCAACAC 840
Qy 841 ATAGAAGAGCTTGAATNGCTGTGACAGTCTTTCATTTCTTTGGCCCAACCTGTG 900
Db 841 ATAGAAGAGCTTGAATNGCTGTGACAGTCTTTCATTTCTTTGGCCCAACCTGTG 900
Qy 901 GAATATCTCAATATTTACAAATTTAAACAATATTTGAAGCATTCGTGAAGAAATTTTACT 960
Db 901 GAATATCTCAATATTTACAAATTTAAACAATATTTGAAGCATTCGTGAAGAAATTTTACT 960
Qy 961 TATTTTAAAGCAGCTTGAAGCATTTGACAAATAGAAACATATACAGAACCAAGTTTTCG 1020
Db 961 TATTTTAAAGCAGCTTGAAGCATTTGACAAATAGAAACATATACAGAACCAAGTTTTCG 1020
Qy 1021 TTTTACAGAGAGCTTTGACACCGTGTCTTGAGATGAGACATTAATGATTTAACCAT 1080
Db 1021 TTTTACAGAGAGCTTTGACACCGTGTCTTGAGATGAGACATTAATGATTTAACCAT 1080
Qy 1081 TCAGATACACCTTTTATACACATGCTGTGCTCCTACGACCAAGACATTCAGATTTTGG 1140
Db 1081 TCAGATACACCTTTTATACACATGCTGTGCTCCTACGACCAAGACATTCAGATTTTGG 1140
Qy 1141 AACTTTACCCGAGACGTTTTCACAGATGATTTTGGAAAAATGTTCCAGTTAGTTAA 1200
Db 1141 AACTTTACCCGAGACGTTTTCACAGATGATTTTGGAAAAATGTTCCAGTTAGTTAA 1200
Qy 1201 TTGGAGACACTTATCTTCAAAAAATGATTAAGAACTTTCAAAAGTATGCTCAG 1260
Db 1201 TTGGAGACACTTATCTTCAAAAAATGATTAAGAACTTTCAAAAGTATGCTCAG 1260
Qy 1261 AGGAAGATATGCTTCTTTGGAATATCTGATGTTAGCTGGAATTTCTTTGGAATCTG 1320
Db 1261 AGGAAGATATGCTTCTTTGGAATATCTGATGTTAGCTGGAATTTCTTTGGAATCTG 1320
Qy 1321 AGACATTAAGAAAACCTGCACTTGGGTGAGAGTATAGTGCTTAATTTGCTTCAAT 1380
Db 1321 AGACATTAAGAAAACCTGCACTTGGGTGAGAGTATAGTGCTTAATTTGCTTCAAT 1380
Qy 1381 ATGCTTACGACCTGTTTTGAGATGTTTACCTCCAGAGATCAAGGTACTGATCTTCC 1440
Db 1381 ATGCTTACGACCTGTTTTGAGATGTTTACCTCCAGAGATCAAGGTACTGATCTTCC 1440

Qy 1441 AGCAATTAATAAAGAGGTTCTTAACAAGTCGTAAACTGGAAGCTTTGCAAGACTC 1500
Db 1441 AGCAATTAATAAAGAGGTTCTTAACAAGTCGTAAACTGGAAGCTTTGCAAGACTC 1500
Qy 1501 AATGTTGCTTTCATATCTTTTAACCTGACCTTCTGGAATGTCGACGTTTAAAGCCTTTCT 1560
Db 1501 AATGTTGCTTTCATATCTTTTAACCTGACCTTCTGGAATGTCGACGTTTAAAGCCTTTCT 1560
Qy 1561 GTATGATCATGATCAAAATTCAGTTTCCACCCATGGCTGATTTTCTCCAGAGCTGC 1620
Db 1561 GTATGATCATGATCAAAATTCAGTTTCCACCCATGGCTGATTTTCTCCAGAGCTGC 1620
Qy 1621 CAGAAATGAGGTCAATTAAGAGGAGCAATTCATTTCAATGTACTGTGACTAAGA 1680
Db 1621 CAGAAATGAGGTCAATTAAGAGGAGCAATTCATTTCAATGTACTGTGACTAAGA 1680
Qy 1681 GAATTTGCAAAAATATATGACCAAGTATCAAGTGAAGTGTTAAGAGGCTGGCTGATTTCT 1740
Db 1681 GAATTTGCAAAAATATATGACCAAGTATCAAGTGAAGTGTTAAGAGGCTGGCTGATTTCT 1740
Qy 1741 TATAGTGGACTACCCAGAAAGTTATAGAGAAAGCCACTAAAGACTTTCACATGTCT 1800
Db 1741 TATAGTGGACTACCCAGAAAGTTATAGAGAAAGCCACTAAAGACTTTCACATGTCT 1800
Qy 1801 GAATTTATCTGCAACATTAACCTGTGATGCTCACCATCGGTGCCACCATGCTGTG 1860
Db 1801 GAATTTATCTGCAACATTAACCTGTGATGCTCACCATCGGTGCCACCATGCTGTG 1860
Qy 1861 GCTGTGATGTCGACCTCCCTCTGCACTTAATTTGATCTGCTGCTGATCTTCAAGATG 1920
Db 1861 GCTGTGATGTCGACCTCCCTCTGCACTTAATTTGATCTGCTGCTGATCTTCAAGATG 1920
Qy 1921 TGCCAGTGAAGCCAGACTCGGCGAGGSCAGAGAAACATACCCTTGAAGAACTCCAAAGA 1980
Db 1921 TGCCAGTGAAGCCAGACTCGGCGAGGSCAGAGAAACATACCCTTGAAGAACTCCAAAGA 1980
Qy 1981 AACCTCAAGTTTCATGCTTTTATTTCAATATGTAAGAACTGATTCGCTGGGTGAAAAGT 2040
Db 1981 AACCTCAAGTTTCATGCTTTTATTTCAATATGTAAGAACTGATTCGCTGGGTGAAAAGT 2040
Qy 2041 GAATTTGATCTTACCTTGAAGAAAGATATATACAGATTTTGTCTTCAAGAGAACTTT 2100
Db 2041 GAATTTGATCTTACCTTGAAGAAAGATATATACAGATTTTGTCTTCAAGAGAACTTT 2100
Qy 2101 GTCCCTGGCAAGAGACTTGTGGAATAATATCACTCACTGATGAGAAGATTACAAGTCC 2160
Db 2101 GTCCCTGGCAAGAGACTTGTGGAATAATATCACTCACTGATGAGAAGATTACAAGTCC 2160
Qy 2161 ATCTTTGTTTTGTCTCCCACTTTGTCCAGATGAGTGTGTCATTAAGAACTGATTTT 2220
Db 2161 ATCTTTGTTTTGTCTCCCACTTTGTCCAGATGAGTGTGTCATTAAGAACTGATTTT 2220
Qy 2221 GCCCATCACAATCTTTTCAAGAGATCTAATACTTAATCCATCTTACTGGAACCC 2280
Db 2221 GCCCATCACAATCTTTTCAAGAGATCTAATACTTAATCCATCTTACTGGAACCC 2280
Qy 2281 ATTCACAGAACAGACTTCCCAACAAGTACCAAGAGCTGATAGACGAGCGG 2340
Db 2281 ATTCACAGAACAGACTTCCCAACAAGTACCAAGAGCTGATAGACGAGCGG 2340
Qy 2341 ACTTATTTGCAGTGGCCCAAGAAAGAAAGCGTGGGCTCTTTTGGGCTTAACATTAGA 2400
Db 2341 ACTTATTTGCAGTGGCCCAAGAAAGAAAGCGTGGGCTCTTTTGGGCTTAACATTAGA 2400
Qy 2401 GCCGCTTTTAAATATGAATTAACACTAGTACTGAAAAACAATGATGTAAAAATCTTAAAAA 2460
Db 2401 GCCGCTTTTAAATATGAATTAACACTAGTACTGAAAAACAATGATGTAAAAATCTTAAAAA 2460
Qy 2461 AATTAGGAATTCACCTTAAGAAAACATTTATTAATCTTGATGATGTAATAGTACAGT 2520
Db 2461 AATTAGGAATTCACCTTAAGAAAACATTTATTTACTTGATGATGTAATAGTACAGT 2520

QY 2521 CGTAACTAAGTCTGTGAGAGTGCCTTCATATCTCATGCTTCAGAGAAAGCTTAAACA 2580
 |||||
 Db 2521 CGTAACTAAGTCTGTGAGAGTGCCTTCATATCTCATGCTTCAGAGAAAGCTTAAACA 2580
 QY 2581 AAAACATGTTTCACTCGGGGAACTGAGCTAGAGCGGTGAGATTAGCTGCAGTTAGAGAC 2640
 |||||
 Db 2581 AAAACATGTTTCACTCGGGGAACTGAGCTAGAGCGGTGAGATTAGCTGCAGTTAGAGAC 2640
 QY 2641 AGCCAGTCTCTTCTGTTTAATCATTAATGTTTCAAATGAACAGTCTCTTTGAGTAA 2700
 |||||
 Db 2641 AGCCAGTCTCTTCTGTTTAATCATTAATGTTTCAAATGAACAGTCTCTTTGAGTAA 2700
 QY 2701 ATGCTCAGTTTTCAGCTCTCTCCAGCTGCTTCCCAATGAGATTCTGTTG 2753
 |||||
 Db 2701 ATGCTCAGTTTTCAGCTCTCTCCAGCTGCTTCCCAATGAGATTCTGTTG 2753
 |||||
 RESULT 3
 ADU23187
 ID ADU23187 standard; cDNA; 2753 BP.
 AC ADU23187;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE Human Toll-like receptor 6 (TLR6) cDNA sequence - SEQ ID 79.
 XX
 KM screening; Toll-like receptor agonist; TLR agonist; gene; ss; TLR6.
 XX
 OS Homo sapiens.
 PN WO2004094671-A2.
 XX
 PD 04-NOV-2004.
 XX
 PF 22-APR-2004; 2004WO-US012788.
 XX
 PR 22-APR-2003; 2003US-0464586P.
 XX
 PR 22-APR-2003; 2003US-0464586P.
 XX
 PA (COLE-) COLEY PHARM GMBH.
 PA (COLE-) COLEY PHARM GROUP INC.
 XX
 PI Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
 XX
 DR WPI; 2004-795573/78.
 XX
 PT Identifying agonists of Toll-like receptor (TLR) signaling activity,
 PT useful therapeutically or prophylactically, comprises contacting an
 PT RPM1826 cell that expresses a TLR with a test compound and measuring TLR
 PT signaling activity.
 XX
 PS Disclosure; SEQ ID NO 79; 342pp; English.
 XX
 PS The invention comprises a screening method for identifying agonists of
 CC Toll-like receptor (TLR) signaling activity. The method involves
 CC contacting an RPM1826 cell (that expresses a TLR) with a test compound,
 CC and measuring a test level of TLR signaling activity, where a test level
 CC that is positive is indicative of a test compound that is a TLR agonist.
 CC The method of the invention is useful for identifying agonists of TLR.
 CC The present nucleic acid represents a TLR cDNA sequence.
 XX
 SQ Sequence 2753 BP; 849 A; 559 C; 507 G; 838 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2753; DB 13; Length 2753;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAATTTGACTCATATCAAGATGCTCTGAGAGAAACAACCTTTAGATAGCCACTGC 60
 |||||
 Db 1 AGAATTTGACTCATATCAAGATGCTCTGAGAGAAACAACCTTTAGATAGCCACTGC 60
 |||||
 QY 61 AACATCATGACCAAGACAAAGAACCTATTTGTTAAAGCTTCATTGTTGCTTATG 120
 |||||

Db 61 AACATCATGACCAAGACAAAGAACCTATTTGTTAAAGCTTCATTGTTGCTTATG 120
 |||||
 QY 121 ATCATTAATAGTTGGAACCAAGAAATCCAGTTCTCCAGCGAAATGAATTTGACATGACAG 180
 |||||
 Db 121 ATCATTAATAGTTGGAACCAAGAAATCCAGTTCTCCAGCGAAATGAATTTGACATGACAG 180
 QY 181 TCAAAAAGAGGCTTATTCATGCTCCAAAGACCTACCGCTGAAAAACCAAGCTTAGAT 240
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 Db 181 TCAAAAAGAGGCTTATTCATGCTCCAAAGACCTACCGCTGAAAAACCAAGCTTAGAT 240
 QY 241 ATGCTCAGAACTACATGCTGAGCTGAGCTGAGTCTCTGACATGAGCTTTCTATCAGAGTGG 300
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 Db 241 ATGCTCAGAACTACATGCTGAGCTGAGCTGAGTCTCTGACATGAGCTTTCTATCAGAGTGG 300
 QY 301 ACAGTTTGAAGCTTTCCCATACAGAAATCCAGCTACTTGAATTAAGTGTTCAGATTC 360
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 Db 301 ACAGTTTGAAGCTTTCCCATACAGAAATCCAGCTACTTGAATTAAGTGTTCAGATTC 360
 QY 361 AACCGAGATTAGATATTTGATTTATCTGATATCCAGTTGCAAAAGATATCCGCGCAT 420
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 Db 361 AACCGAGATTAGATATTTGATTTATCTGATATCCAGTTGCAAAAGATATCCGCGCAT 420
 QY 421 CCTATTGAGTTTCAGGCAATTTAGATCTCTCAATCAATGATTTTCAAGGCCCTGCCATC 480
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 Db 421 CCTATTGAGTTTCAGGCAATTTAGATCTCTCAATCAATGATTTTCAAGGCCCTGCCATC 480
 QY 481 TGTAAAGAAATTTGCAACTTATCACAAGTAAATTTCTTGAGATTGATGATGAAAGCTG 540
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 Db 481 TGTAAAGAAATTTGCAACTTATCACAAGTAAATTTCTTGAGATTGATGATGAAAGCTG 540
 QY 541 CAAAAATTAGATTGCTGCTGCAATTTGCTCACTTGCACTTAAGTATATCTTCTGATTTA 600
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 Db 541 CAAAAATTAGATTGCTGCTGCAATTTGCTCACTTGCACTTAAGTATATCTTCTGATTTA 600
 QY 601 AGAAATTTATATATTAAGAAAGAAATAGACAGAGAACTACAAATTTCTGATSCAAAAACC 660
 |||||
 Db 601 AGAAATTTATATATTAAGAAAGAAATAGACAGAGAACTACAAATTTCTGATSCAAAAACC 660
 QY 661 CTTCACCTTGTGTTTTCACCCAACTAGTTTATTTGCTATCCAAAGTACATATCACTTAT 720
 |||||
 Db 661 CTTCACCTTGTGTTTTCACCCAACTAGTTTATTTGCTATCCAAAGTACATATCACTTAT 720
 QY 721 ACTTTAGGCTGCTTACCACTGACTAATTTAATTTGAATGATGACACTGTCAAGTTTC 780
 |||||
 Db 721 ACTTTAGGCTGCTTACCACTGACTAATTTAATTTGAATGATGACACTGTCAAGTTTC 780
 QY 781 ATTAAATTTTATGCAAGCTCAGCAGAGGTTCAACCTTACGAAATTTTACCTCAACAC 840
 |||||
 Db 781 ATTAAATTTTATGCAAGCTCAGCAGAGGTTCAACCTTACGAAATTTTACCTCAACAC 840
 QY 841 ATAGAAAGACTTGGAAATGCGTGTGAGAGTCTTCAATTTCTTGCCCAAAACCTGTG 900
 |||||
 Db 841 ATAGAAAGACTTGGAAATGCGTGTGAGAGTCTTCAATTTCTTGCCCAAAACCTGTG 900
 QY 901 GAATATCTCAATTTTACAAATTTAACAATATTTGAAGCAATTTCTGGAAGAAATTTTACT 960
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 Db 901 GAATATCTCAATTTTACAAATTTAACAATATTTGAAGCAATTTCTGGAAGAAATTTTACT 960
 QY 961 TATTTCAAAAGCACTTGAAGCAATTTGACATATGACATATCAGAACCAAGTTTCTG 1020
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 Db 961 TATTTCAAAAGCACTTGAAGCAATTTGACATATGACATATCAGAACCAAGTTTCTG 1020
 QY 1021 TTTTACAGACAGCTTTGTACACCGTGTGTTTCTGAGATGAACATATGATGTAAACAT 1080
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 Db 1021 TTTTACAGACAGCTTTGTACACCGTGTGTTTCTGAGATGAACATATGATGTAAACAT 1080
 QY 1081 TCAATATACACTTTTATATACATGCTGTGCTCTGATGACCAACACATTTCAAGTTTGG 1140
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 Db 1081 TCAATATACACTTTTATATACATGCTGTGCTCTGATGACCAACACATTTCAAGTTTGG 1140
 QY 1141 AACTTATCCCAAGAGCTTTTACAGATAGTATTTTGAATAATGTCCAGCTTGTATTA 1200
 |||||

Db 1141 AACTTACCCAGACGTTTTCACAGATAGTATTTTGA AAAATGTTCCAGCTTACTGTTAA 1200
 Qy 1201 TTGGAGACCTATCTTACAAAAAATGGATTAAAAAGCCTTTTCAAAAGTAGTCTCATG 1260
 Db 1201 TTGGAGACCTATCTTACAAAAAATGGATTAAAAAGCCTTTTCAAAAGTAGTCTCATG 1260
 Qy 1261 ACGAAGATATGCTCTTTTGGAAATACTGATGTTAGCTGGAATTTCTTTGGAATCTGGT 1320
 Db 1261 ACGAAGATATGCTCTTTTGGAAATACTGATGTTAGCTGGAATTTCTTTGGAATCTGGT 1320
 Qy 1321 AGACATTAAGAAACGTCAGCTGGGTGAGAGATATAGTGTTAAATTTGTTCTTCAAT 1380
 Db 1321 AGACATTAAGAAACGTCAGCTGGGTGAGAGATATAGTGTTAAATTTGTTCTTCAAT 1380
 Qy 1381 ATGCTTACTGACTGTGTTTCAGATGTTTACCTCCAGAGATCAAGTACTTATCTTAC 1440
 Db 1381 ATGCTTACTGACTGTGTTTCAGATGTTTACCTCCAGAGATCAAGTACTTATCTTAC 1440
 Qy 1441 AGCAATTAATAAAGACGTTCTTAAACAAATGTTAAACCTGGAAGCTTTGCAAGAACTC 1500
 Db 1441 AGCAATTAATAAAGACGTTCTTAAACAAATGTTAAACCTGGAAGCTTTGCAAGAACTC 1500
 Qy 1501 AATGTTGCTTCAATTTCTTAACTGACCTTCCGATGTTGAGAGCTTTAGCAGCCTTCT 1560
 Db 1501 AATGTTGCTTCAATTTCTTAACTGACCTTCCGATGTTGAGAGCTTTAGCAGCCTTCT 1560
 Qy 1561 GTATTGATCATTCATCAATTCAGTTTCCACCCATCGGCTGATTTCTTCCAGAGCTGC 1620
 Db 1561 GTATTGATCATTCATCAATTCAGTTTCCACCCATCGGCTGATTTCTTCCAGAGCTGC 1620
 Qy 1621 CAGAAATGAGTCAATTAAGACGAGGAAATCCATTCCAAATGTAACCTGTGAGCTAAGA 1680
 Db 1621 CAGAAATGAGTCAATTAAGACGAGGAAATCCATTCCAAATGTAACCTGTGAGCTAAGA 1680
 Qy 1681 GAATTTGTCAAAAATTTAGACCAAGATCAAGTAAAGTATGAGGAGCTGGCCTGATTTCT 1740
 Db 1681 GAATTTGTCAAAAATTTAGACCAAGATCAAGTAAAGTATGAGGAGCTGGCCTGATTTCT 1740
 Qy 1741 TATAAGTGTGACTACCCAGAAAGTTATAGAGAAAGCCCACTAAAGACTTTTCAATGTCT 1800
 Db 1741 TATAAGTGTGACTACCCAGAAAGTTATAGAGAAAGCCCACTAAAGACTTTTCAATGTCT 1800
 Qy 1801 GAATTAATCTGCAACATACTCTGTGATGTCACCATGCTGGTCCCAATGCTGTGTTG 1860
 Db 1801 GAATTAATCTGCAACATACTCTGTGATGTCACCATGCTGGTCCCAATGCTGTGTTG 1860
 Qy 1861 GCTGTGACTGTGACCTCTCTGTCATCTTCTGATGTTGATCTGAGATGTTG 1920
 Db 1861 GCTGTGACTGTGACCTCTCTGTCATCTTCTGATGTTGATCTGAGATGTTG 1920
 Qy 1921 TGCCAGTGAACCCAGACTCGGCGCAGAGGCGAGGAACATACCTTAGAAGAACTCCAAAGA 1980
 Db 1921 TGCCAGTGAACCCAGACTCGGCGCAGAGGCGAGGAACATACCTTAGAAGAACTCCAAAGA 1980
 Qy 1981 AACCTTCAGTTTCATGCTTTTATTTTCATATAGTGAACATGATTCTGCTGGTGAAGT 2040
 Db 1981 AACCTTCAGTTTCATGCTTTTATTTTCATATAGTGAACATGATTCTGCTGGTGAAGT 2040
 Qy 2041 GAATTTGTTTGTCTTACCTTAGAAAAAAGAAATATACATGTTTGTCTTATAGAGGAATCTT 2100
 Db 2041 GAATTTGTTTGTCTTACCTTAGAAAAAAGAAATATACATGTTTGTCTTATAGAGGAATCTT 2100
 Qy 2101 GTCCCTGGCAAGAGACTGTGGAAGAAATATCATCAATGATGATGAGAAAGTTTCAAGTCC 2160
 Db 2101 GTCCCTGGCAAGAGACTGTGGAAGAAATATCATCAATGATGATGAGAAAGTTTCAAGTCC 2160
 Qy 2161 ATCTTTGTTTGTCTTCCAACTTTGTCCAGAGTGAATGGGCACTTATCAAACTTATTTT 2220
 Db 2161 ATCTTTGTTTGTCTTCCAACTTTGTCCAGAGTGAATGGGCACTTATCAAACTTATTTT 2220
 Qy 2221 GCCCATCAAAATCTCTTTTATGAGAGATCTAATACTTAATCTCTATCTTATCGGAACCC 2280
 Db 2221 GCCCATCAAAATCTCTTTTATGAGAGATCTAATACTTAATCTCTATCTTATCGGAACCC 2280

Qy 2281 ATTCCAGAAACAGATTTCCCAAGATGACCAAGAAAGCTTGAAGGCTCTCATGACGACGGG 2340
 Db 2281 ATTCCAGAAACAGATTTCCCAAGATGACCAAGAAAGCTTGAAGGCTCTCATGACGACGGG 2340
 Qy 2341 ACTTATTTGCAATGGGCCCCAAGAGAAAGCAAAAGGTGGGCTCTTTTGGGCTTAACATTAGA 2400
 Db 2341 ACTTATTTGCAATGGGCCCCAAGAGAAAGCAAAAGGTGGGCTCTTTTGGGCTTAACATTAGA 2400
 Qy 2401 GCCGCTTTTAAATGAAATTAACACTAGTCACTGAAAACAATGATGTAATCTTTAAAAA 2460
 Db 2401 GCCGCTTTTAAATGAAATTAACACTAGTCACTGAAAACAATGATGTAATCTTTAAAAA 2460
 Qy 2461 AATTTAGAAATTTCACTTAAGAAACCTTTTATTTACTGATGATGGTGAATAGTACAGT 2520
 Db 2461 AATTTAGAAATTTCACTTAAGAAACCTTTTATTTACTGATGATGGTGAATAGTACAGT 2520
 Qy 2521 CGTAACTAATCTGTCGAGAGGAGGCTCCATTAATCCATGACCTTCAAGAAAGACTTAACA 2580
 Db 2521 CGTAACTAATCTGTCGAGAGGAGGCTCCATTAATCCATGACCTTCAAGAAAGACTTAACA 2580
 Qy 2581 AAACAATGTTTCATCTGAGGAACTGAGCTAGGCGGTGAGTTAGCTGCGCAGTTAGAGAC 2640
 Db 2581 AAACAATGTTTCATCTGAGGAACTGAGCTAGGCGGTGAGTTAGCTGCGCAGTTAGAGAC 2640
 Qy 2641 AGCCAGTCTCTTCTGTTTATCATTAATGTTTCAAAATGTAACAGTCTTTTGAAGTAA 2700
 Db 2641 AGCCAGTCTCTTCTGTTTATCATTAATGTTTCAAAATGTAACAGTCTTTTGAAGTAA 2700
 Qy 2701 ATGCTCAATTTTTCAGTCTCTCTCCATCTGCTTCCAAATGGAATCTGTTG 2753
 Db 2701 ATGCTCAATTTTTCAGTCTCTCTCCATCTGCTTCCAAATGGAATCTGTTG 2753
 RESULT 4
 ADX06215
 ID ADX06215 standard; DNA, 2753 BP.
 XX
 AC ADX06215;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 780.
 XX
 KW cytosolic; cyclin-dependent kinase; cdk; biomarker; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN W02005012875-A2.
 XX
 PD 10-FEB-2005.
 XX
 PF 29-JUL-2004; 2004MO-US024424.
 XX
 PR 29-JUL-2003; 2003US-0490890P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
 XX
 DR WPI; 2005-163068/17.
 XX
 DR P-PSDB; ADX06216.
 XX
 PT Biomarkers useful for predicting or determining the response of a mammal
 PT to a cancer treatment comprising administration of a modulator of cyclin-
 PT dependent kinase activity.
 XX
 PS Claim 5; SEQ ID NO 780; 141bp; English.
 XX
 CC This invention describes a novel method of predicting or determining
 CC whether a mammal will respond or is responding to an anti-cancer agent
 CC that modulates cyclin-dependent kinase (cdk) activity. The method
 CC comprises measuring the level of one or more biomarkers selected from

CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC NO:1246 (Genbank EST M28729) is especially preferred). The method of the
CC invention is utilized in a kit for determining or predicting whether
CC patient would be susceptible or resistant to treatment by an agent.
CC modulating cdk activity. The invention also describes a method for
CC utilizing individualized genetic profiles for treating diseases and
CC disorders based on patient's response and molecular level, specialized
CC microarrays comprising the biomarkers described, antibodies directed
CC against the biomarkers and a cell culture model to identify biomarkers.
CC The cdk modulator is preferably N-5-[(5-(1,1-dimethylethyl)-2-
CC oxazolyl)methyl]thiol-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
CC tartaric acid salt. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from Wipo at ftp.wipo.int/pub/published not sequences. This
CC sequence encodes a biomarker used in the method of the invention.
XX
SQ Sequence 2753 BP; 849 A; 559 C; 507 G; 838 T; 0 U; 0 Other;

Query Match 100.0%; Score 2753; DB 14; Length 2753;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAATTTGAGCTCATATCAAGATGCTTGAGAGAGAACACCCTTAGAGTACCACTGC 60
DB 1 AGAATTTGAGCTCATATCAAGATGCTTGAGAGAGAACACCCTTAGAGTACCACTGC 60
QY 61 AACATCAGACCCAAAGACAAAGAACCTATGTTAAAGCTTCATTGTTGGCTTATG 120
DB 61 AACATCAGACCCAAAGACAAAGAACCTATGTTAAAGCTTCATTGTTGGCTTATG 120
QY 121 ATCAATATATGTTGGAACAGAAATCCAGTTCTCCGACGGAATGAAATTTGACATAGACAAG 180
DB 121 ATCAATATATGTTGGAACAGAAATCCAGTTCTCCGACGGAATGAAATTTGACATAGACAAG 180
QY 181 TCAAAAAGAGGCTTATTCATGTTCCAAAAGACCTACCGCTGAAAAACCAAGTCTTAGAT 240
DB 181 TCAAAAAGAGGCTTATTCATGTTCCAAAAGACCTACCGCTGAAAAACCAAGTCTTAGAT 240
QY 241 ATGCTCAGAACTAATGCTGAGGCTTCAAGGCTCTGACATAGAGCTTTCTATCAAGATTG 300
DB 241 ATGCTCAGAACTAATGCTGAGGCTTCAAGGCTCTGACATAGAGCTTTCTATCAAGATTG 300
QY 301 ACAGTTTGGAGACTTCCCATTAAGAAATCCAGTACTGATTTTAAAGTGTTCAGATTC 360
DB 301 ACAGTTTGGAGACTTCCCATTAAGAAATCCAGTACTGATTTTAAAGTGTTCAGATTC 360
QY 361 AACGAGATTTAGATATTTGGATTATCTCATATCAGTTGCCAAAAGATATCTGCCAT 420
DB 361 AACGAGATTTAGATATTTGGATTATCTCATATCAGTTGCCAAAAGATATCTGCCAT 420
QY 421 CCTATTTGAGATTTGAGGCTTAAATCTCTCATTCATGATTTCAAGGCCCTGCCATC 480
DB 421 CCTATTTGAGATTTGAGGCTTAAATCTCTCATTCATGATTTCAAGGCCCTGCCATC 480
QY 481 TGTAAAGAAATTTGGCACTTATCAACAGTGAATTTCTGGGATGAGTGAATGAAGCTG 540
DB 481 TGTAAAGAAATTTGGCACTTATCAACAGTGAATTTCTGGGATGAGTGAATGAAGCTG 540
QY 541 CAAAATTTAGATTGCTGCCAATTGCTCATCTTGACCTTAAGTTATATCTTCTGGAATTTA 600
DB 541 CAAAATTTAGATTGCTGCCAATTGCTCATCTTGACCTTAAGTTATATCTTCTGGAATTTA 600
QY 601 AGAAATTTATATTAAGAAAGAAATGAGACAGAAATCTCAAAATTTCTAAGTGAACAAAAC 660
DB 601 AGAAATTTATATTAAGAAAGAAATGAGACAGAAATCTCAAAATTTCTAAGTGAACAAAAC 660
QY 661 CTTCACCTTTGTTTTCACCAACTAGTTATTCGCTATCCAAAGTGAACATATCAGTTAT 720
DB 661 CTTCACCTTTGTTTTCACCAACTAGTTATTCGCTATCCAAAGTGAACATATCAGTTAT 720
QY 721 ACTTTAGGCTGCTTACAACTGACTAATATTAATTTGAATGATGACAACTGTCAAGTTTTC 780
DB 721 ACTTTAGGCTGCTTACAACTGACTAATATTAATTTGAATGATGACAACTGTCAAGTTTTC 780

QY 781 ATTAATTTTATCAGAACTCCAGAGGTTCAACCTTACGATTTTACCTCAACGAC 840
DB 781 ATTAATTTTATCAGAACTCCAGAGGTTCAACCTTACGATTTTACCTCAACGAC 840
QY 841 ATAGAAAGACTTGGAAATGCTGCTGACAGCTTTTCATTTCTTTGGCCAAACCTG 900
DB 841 ATAGAAAGACTTGGAAATGCTGCTGACAGCTTTTCATTTCTTTGGCCAAACCTG 900
QY 901 GAATATCTCAATATTTACATTTTAACAATATTTGAAGACATTCGTGAAGAAATTTACT 960
DB 901 GAATATCTCAATATTTACATTTTAACAATATTTGAAGACATTCGTGAAGAAATTTACT 960
QY 961 TATTTTAAAGCACTTGAAGACATTTGACATATGAAACCATTAACCAATTTTCTG 1020
DB 961 TATTTTAAAGCACTTGAAGACATTTGACATATGAAACCATTAACCAATTTTCTG 1020
QY 1021 TTTTCAAGACAGCTTTGTACACCGTGTGTTTCTGATGATGAACATTTATGATTAACATT 1080
DB 1021 TTTTCAAGACAGCTTTGTACACCGTGTGTTTCTGATGATGAACATTTATGATTAACATT 1080
QY 1081 TCAGATACACCTTTTATACACATGCTGTGCTCATGACCAAGACATTCAGATTTTGG 1140
DB 1081 TCAGATACACCTTTTATACACATGCTGTGCTCATGACCAAGACATTCAGATTTTGG 1140
QY 1141 AACTTTACCGAAGAGCTTTTACAGATAGTATTTTGAAGAAATGTTCCACCTTACTTAA 1200
DB 1141 AACTTTACCGAAGAGCTTTTACAGATAGTATTTTGAAGAAATGTTCCACCTTACTTAA 1200
QY 1201 TTGAGACACTTATCTTCAAAAAATGATTTAAAGACCTTTTCAAGTAGTCTCATG 1260
DB 1201 TTGAGACACTTATCTTCAAAAAATGATTTAAAGACCTTTTCAAGTAGTCTCATG 1260
QY 1261 AGAAGATATGCTCTTTTGGAAATCTGATGTTAGCTGGAATCTGCT 1320
DB 1261 AGAAGATATGCTCTTTTGGAAATCTGATGTTAGCTGGAATCTGCT 1320
QY 1321 AGACATTAAGAAACTGACCTTTGGTGAAGATATAGTGTGTTAAATTTGCTTCAAT 1380
DB 1321 AGACATTAAGAAACTGACCTTTGGTGAAGATATAGTGTGTTAAATTTGCTTCAAT 1380
QY 1381 ATGCTTACGACTGCTTTTCAAGATGTTTACCTCCAGATCAAGTACTGATCTTAC 1440
DB 1381 ATGCTTACGACTGCTTTTCAAGATGTTTACCTCCAGATCAAGTACTGATCTTAC 1440
QY 1441 AGCAATTAATTAAGAGGCTTCTTAACCAAGTCTGTAACCTTTGCAAGATCTC 1500
DB 1441 AGCAATTAATTAAGAGGCTTCTTAACCAAGTCTGTAACCTTTGCAAGATCTC 1500
QY 1501 AATGTTGCTTTCAATTTCTTTAATCTGACCTTCTGATGTGCAAGCTTTTCT 1560
DB 1501 AATGTTGCTTTCAATTTCTTTAATCTGACCTTCTGATGTGCAAGCTTTTCT 1560
QY 1561 GTATGATCATTTGATCAAAATTCAGTTTCCACCATGAGGCTGATTTCTTCAGAGCTGC 1620
DB 1561 GTATGATCATTTGATCAAAATTCAGTTTCCACCATGAGGCTGATTTCTTCAGAGCTGC 1620
QY 1621 CAGAAATGAGTCAATTAAGACAGGGGACATTCATTTCAATGTATCTGTGAGCTAAGA 1680
DB 1621 CAGAAATGAGTCAATTAAGACAGGGGACATTCATTTCAATGTATCTGTGAGCTAAGA 1680
QY 1681 GAATTTGCAAAATATATGACCAAGTATCAAGTGAAGTGTGAGAGGCTGCTGATTTCT 1740
DB 1681 GAATTTGCAAAATATATGACCAAGTATCAAGTGAAGTGTGAGAGGCTGCTGATTTCT 1740
QY 1741 TATAAGTGTGACTCCAGAAAGTTATGAGAAAGCCCACTAAGAACTTTCAACATGCT 1800
DB 1741 TATAAGTGTGACTCCAGAAAGTTATGAGAAAGCCCACTAAGAACTTTCAACATGCT 1800
QY 1801 GAATTTATCTGCAACATATCTGCTGATCTGATCCATCGGTGCCACATCTGCTGTTG 1860
DB 1801 GAATTTATCTGCAACATATCTGCTGATCTGATCCATCGGTGCCACATCTGCTGTTG 1860

181 TCAAAAAGAGTCTTATTCATGTTCCAAAAGACCTACCGCTGAAAACCAAGCTTAGAT 240
182 TCAAAAAGAGTCTTATTCATGTTCCAAAAGACCTACCGCTGAAAACCAAGCTTAGAT 241
QY 241 ATGTCTCAGACCTACATCGCTGAGCTTGAGTCTCTGACATGAGCTTCTATCAGAGTTG 300
Db 242 ATGTCTCAGACCTACATCGCTGAGCTTGAGTCTCTGACATGAGCTTCTATCAGAGTTG 301
QY 301 ACAGTTTGGAGCTTCCCATTAACAGAACCTGAGCTTGAATTAAGTGTTCAGATTC 360
Db 302 ACAGTTTGGAGCTTCCCATTAACAGAACCTGAGCTTGAATTAAGTGTTCAGATTC 361
QY 361 AACCGAGATTTAGAAATTTGGATTTATCTCAATATCAGTTGCAAAAGATTCCTGCAT 420
Db 362 AACCGAGATTTAGAAATTTGGATTTATCTCAATATCAGTTGCAAAAGATTCCTGCAT 421
QY 421 CCTATTTGAGTTCAGGCAATTTAGATCTCTCATTCATGATTTTCAAGGCCCTGCCATC 480
Db 422 CCTATTTGAGTTCAGGCAATTTAGATCTCTCATTCATGATTTTCAAGGCCCTGCCATC 481
QY 481 TGTATGGAATTTGGCACTTATCACTGAATTTCTTGGAGTTGAGTCTATGAAGCTG 540
Db 482 TGTATGGAATTTGGCACTTATCACTGAATTTCTTGGAGTTGAGTCTATGAAGCTG 541
QY 541 CAAAAATTAGATTTGCTGCCAATTTGCTCACTTGCATCTAAGTTATATCTCTGAGTTTA 600
Db 542 CAAAAATTAGATTTGCTGCCAATTTGCTCACTTGCATCTAAGTTATATCTCTGAGTTTA 601
QY 601 AGAAATTTATATATAAAGAAAATGAGACAGAAAGTCTACAAATTCGTAATCCAAAACC 660
Db 602 AGAAATTTATATATAAAGAAAATGAGACAGAAAGTCTACAAATTCGTAATCCAAAACC 661
QY 661 CTTCACCTTTGTTTTCACCCCACTAGTTTATTCGCTATCCAAAGTGAACATATCAGTTAAT 720
Db 662 CTTCACCTTTGTTTTCACCCCACTAGTTTATTCGCTATCCAAAGTGAACATATCAGTTAAT 721
QY 721 ACTTTAGGGTGCTTCAACTGACTGACTATATTAATTAATGAATGAGACAACTGCAAGTTTC 780
Db 722 ACTTTAGGGTGCTTCAACTGACTGACTATATTAATTAATGAATGAGACAACTGCAAGTTTC 781
QY 781 ATTTAAATTTTATATCAGAACTCACAGAGGTTCAACTGAAATTTTACCTTCAACAC 840
Db 782 ATTTAAATTTTATATCAGAACTCACAGAGGTTCAACTGAAATTTTACCTTCAACAC 841
QY 841 ATGAAAAGCACTTGGAAATGCTGCTGAGAGTCTTTCAAATTTCTTGGCCCAAACTGTG 900
Db 842 ATGAAAAGCACTTGGAAATGCTGCTGAGAGTCTTTCAAATTTCTTGGCCCAAACTGTG 901
QY 901 GAATATCTCAATTTTACAATTTTAACTAATTAATGAAGCATTCGTAAGAAAGATTTTACT 960
Db 902 GAATATCTCAATTTTACAATTTTAACTAATTAATGAAGCATTCGTAAGAAAGATTTTACT 961
QY 961 TATTTTAAAGCAGACTTGAAGACATTTGACATATGAAACATATCAGAACCAAGTTTTCG 1020
Db 962 TATTTTAAAGCAGACTTGAAGACATTTGACATATGAAACATATCAGAACCAAGTTTTCG 1021
QY 1021 TTTTTCACGACGCTTTTGAACCGGTGTTTCTGAGATGACATTAATGATTTAACCAT 1080
Db 1022 TTTTTCACGACGCTTTTGAACCGGTGTTTCTGAGATGACATTAATGATTTAACCAT 1081
QY 1081 TCAGATACACCTTTTATACATGCTGCTGCTCACTGACCAAGACCAATTCAGTTTTCG 1140
Db 1082 TCAGATACACCTTTTATACATGCTGCTGCTCACTGACCAAGACCAATTCAGTTTTCG 1141
QY 1141 AACTTTACCGAAGCGTTTTCACAGATGATATTTTGAAGAAATGTTTCCAGTTAGTTAA 1200
Db 1142 AACTTTACCGAAGCGTTTTCACAGATGATATTTTGAAGAAATGTTTCCAGTTAGTTAA 1201
QY 1201 TTGAGACACTTATCTTACAAAAAATGATTTAAAGACCTTTTCAAGTAGTCTCATG 1260
Db 1202 TTGAGACACTTATCTTACAAAAAATGATTTAAAGACCTTTTCAAGTAGTCTCATG 1261

QY 1261 ACGAAGATATGCTCTTCTTTGAAAATACTGATGTTAGCTGGAATCTTTGGAATCTGCT 1320
Db 1262 ACGAAGATATGCTCTTCTTTGAAAATACTGATGTTAGTGTGGAATCTTTGGAATCTGCT 1321
QY 1321 AGACATTAAGAAAAGCTGCACTTGGGTGAGATATGAGTGTAAATTTGTCTTCAAT 1380
Db 1322 AGACATTAAGAAAAGCTGCACTTGGGTGAGATATGAGTGTAAATTTGTCTTCAAT 1381
QY 1381 ATGCTTACGACTGTTTTCAGATGTTTACTCCCAAGATCAAGGTACTTGAATCTTCCAC 1440
Db 1382 ATGCTTACGACTGTTTTCAGATGTTTACTCCCAAGATCAAGGTACTTGAATCTTCCAC 1441
QY 1441 ACCAATTAAGAAAAGCGTCTTCTTAAACAGTCTGTAATACTGAAAGCTTTGCAAGACTC 1500
Db 1442 ACCAATTAAGAAAAGCGTCTTCTTAAACAGTCTGTAATACTGAAAGCTTTGCAAGACTC 1501
QY 1501 AATGTTGCTTTCAATTTCTTTTAACTGACCTTCTGAGATGTCAGACTTTAGACGCTTTC 1560
Db 1502 AATGTTGCTTTCAATTTCTTTTAACTGACCTTCTGAGATGTCAGACTTTAGACGCTTTC 1561
QY 1561 GTATGATCATGATGACAAATTCAGTTTCCCAACCATGCGCTGATTTCTTCCAGAGCTGC 1620
Db 1562 GTATGATCATGATGACAAATTCAGTTTCCCAACCATGCGCTGATTTCTTCCAGAGCTGC 1621
QY 1621 CAGAAGATGAGGTCAATTAAGCAGGGGCAATTCATTCATGATGATCTGTAGCTTAA 1680
Db 1622 CAGAAGATGAGGTCAATTAAGCAGGGGCAATTCATTCATGATGATCTGTAGCTTAA 1681
QY 1681 GAATTTGTCAAAATATATAGACCAAGTATCAAGTGAAGTGTTAAGAGGCTGAGCTGATTC 1740
Db 1682 GAATTTGTCAAAATATATAGACCAAGTATCAAGTGAAGTGTTAAGAGGCTGAGCTGATTC 1741
QY 1741 TATATGCTGATACCCAGAAAATTTATAGAGAACCCCACTTAAAGACTTTACATGCTCT 1800
Db 1742 TATATGCTGATACCCAGAAAATTTATAGAGAACCCCACTTAAAGACTTTACATGCTCT 1801
QY 1801 GAATATCTCTGCAATTAATCTGCTGATCTGCATCTGCACATGAGTGGCCACATGCTGGGTG 1860
Db 1802 GAATATCTCTGCAATTAATCTGCTGATCTGCATCTGCACATGAGTGGCCACATGCTGGGTG 1861
QY 1861 GCTGTGACTGTGACCTCCCTCTGCAATCTTGAATCTGCTGCTGATCTCAGATGCTG 1920
Db 1862 GCTGTGACTGTGACCTCCCTCTGCAATCTTGAATCTGCTGCTGATCTCAGATGCTG 1921
QY 1921 TGCAGTGAAGCCCAAGCTTCGCGGCGAGGGCCAGAAACATACCTTGAAGAACTCCAAAGA 1980
Db 1922 TGCAGTGAAGCCCAAGCTTCGCGGCGAGGGCCAGAAACATACCTTGAAGAACTCCAAAGA 1981
QY 1981 AACCTCAGTTTCAATGCTTTTATTTTCAATATGTAAGATGATTCGCTGGGTGAAGAT 2040
Db 1982 AACCTCAGTTTCAATGCTTTTATTTTCAATATGTAAGATGATTCGCTGGGTGAAGAT 2041
QY 2041 GAATTTGTAACCTTACCTTGAAGAAAAGATATACAGATTTGTCTTATGAGAGAACTTT 2100
Db 2042 GAATTTGTAACCTTACCTTGAAGAAAAGATATACAGATTTGTCTTATGAGAGAACTTT 2101
QY 2101 GTCCCTGGCAGAGACTTGTGAAAAATATCATCACTGATTTGAGAAGATTTCAAGTCC 2160
Db 2102 GTCCCTGGCAGAGACTTGTGAAAAATATCATCACTGATTTGAGAAGATTTCAAGTCC 2161
QY 2161 ATCTTTGTTTGTCTCCCAACTTTGTCCAGAGTGAAGTGTGCATTTAGAACTCATTTT 2220
Db 2162 ATCTTTGTTTGTCTCCCAACTTTGTCCAGAGTGAAGTGTGCATTTAGAACTCATTTT 2221
QY 2221 GCCCATCAAAATCTCTTTCATGAAAGATCTAATACTTAATCTCATCTTACGTGAACCC 2280
Db 2222 GCCCATCAAAATCTCTTTCATGAAAGATCTAATACTTAATCTCATCTTACGTGAACCC 2281
QY 2281 ATTCCACGAAACAGATTTCCCAACAGTACCAACAGCTGAAGGCTCTATGACGAGGG 2340
Db 2282 ATTCCACGAAACAGATTTCCCAACAGTACCAACAGCTGAAGGCTCTATGACGAGGG 2341
QY 2341 ACTTATTTGAGTGGCCCAAGGAGAAAGCAAAAGTGGGCTCTTTTGGGCTTAACATTA 2400

|||||
Db 2342 ACTATTGTCAGTGGCCCAAGAGAAAGCAAACTGGGCTCTTTGGGCTTAACATTAGA 2401
QY 2401 GCCCGTTTAAATATGAAATTAACACTAGCTGAAAAAATGATGAAATCTTAAAAA 2460
Db 2402 GCCCGTTTAAATATGAAATTAACACTAGCTGAAAAAATGATGAAATCTTAAAAA 2461
QY 2461 AATTAGGAAATTCACCTTAAGAAACCATTAATTTACTTGATGATGTAATAGTACAGT 2520
Db 2462 AATTAGGAAATTCACCTTAAGAAACCATTAATTTACTTGATGATGTAATAGTACAGT 2521
QY 2521 CGTAACTAGTCTGGAAGTCCCTCATTTATCTCATGCTTCCGAAAGACTTAAACA 2580
Db 2522 CGTAACTAGTCTGGAAGTCCCTCATTTATCTCATGCTTCCGAAAGACTTAAACA 2581
QY 2581 AAACAACTGTTTCATGCGGGAACCTGAGCTAGCGGGAAGTTAGCTGCACTTGAAGC 2640
Db 2582 AAACAACTGTTTCATGCGGGAACCTGAGCTAGCGGGAAGTTAGCTGCACTTGAAGC 2641
QY 2641 AGCCAGTCTCTTCTGTTTATCATTAATGTTTCAAAATGAAACAGTCTCTTTGAGTAA 2700
Db 2642 AGCCAGTCTCTTCTGTTTATCATTAATGTTTCAAAATGAAACAGTCTCTTTGAGTAA 2701
QY 2701 ATGCTGAGTTTTCAGTCTCTCTCCACTCTGCTTCCAAATGATGATTCTGTTG 2753
Db 2702 ATGCTGAGTTTTCAGTCTCTCTCCACTCTGCTTCCAAATGATGATTCTGTTG 2754

RESULT 6

ADU23186 ID ADU23186 standard; cDNA; 2760 BP.

ADU23186;

27-JAN-2005 (first entry)

Human Toll-like receptor 6 (TLR6) cDNA sequence - SEQ ID 78.

screening; Toll-like receptor agonist; TLR agonist; gene; ss; TLR6.

Homo sapiens.

WO2004094671-A2.

04-NOV-2004.

22-APR-2004; 2004WO-US012788.

22-APR-2003; 2003US-0464586P.

22-APR-2003; 2003US-0464588P.

(COLE-) COLEY PHARM GMBH.

(COLE-) COLEY PHARM GROUP INC.

Volmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;

WPI, 2004-795573/78.

Identifying agonists of Toll-like receptor (TLR) signaling activity, useful therapeutically or prophylactically, comprises contacting an RPM18226 cell that expresses a TLR with a test compound and measuring TLR signaling activity.

Disclosure: SEQ ID NO 78; 342pp; English.

The invention comprises a screening method for identifying agonists of Toll-like receptor (TLR) signaling activity. The method involves contacting an RPM18226 cell (that expresses a TLR) with a test compound, and measuring a test level of TLR signaling activity, where a test level that is positive is indicative of a test compound that is a TLR agonist. The method of the invention is useful for identifying agonists of TLR. The present nucleic acid represents a TLR cDNA sequence.

SQ Sequence 2760 BP; 850 A; 560 C; 511 G; 838 T; 0 U; 1 Other;

Query Match 99.8%; Score 2748.8; DB 13; Length 2760;

Best Local Similarity 99.9%; Pred. No. 0; Matches 2750; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 AGAATTTGAGCTCATATCAGATGCTGAAAGAAACACCCTTTAGATAGCACCTGC 60
2 AGAATTTGAGCTCATATCAGATGCTGAAAGAAACACCCTTTAGATAGCACCTGC 61
QY 61 AACATCATGACCAAGACCAAGAACTATGTTTAAAGCTTCCATTTTGGCTTATG 120
Db 62 AACATCATGACCAAGACCAAGAACTATGTTTAAAGCTTCCATTTTGGCTTATG 121
QY 121 ATCATTAATAGTTGGAACAGAAATCCAGTCTCCAGCGAAATGAATTCAGTACAA 180
Db 122 ATCATTAATAGTTGGAACAGAAATCCAGTCTCCAGCGAAATGAATTCAGTACAA 181
QY 181 TCAGAAAGAGGCTTATTCATGTTCCAAAGACCTACCGCTGAAACCAAGCTTAGAT 240
Db 182 TCAGAAAGAGGCTTATTCATGTTCCAAAGACCTACCGCTGAAACCAAGCTTAGAT 241
QY 241 ATGCTGAGACTCATGCTGAGCTTCAAGCTCTGACATGAGCTTCTATCAGAGTTG 300
Db 242 ATGCTGAGACTCATGCTGAGCTTCAAGCTCTGACATGAGCTTCTATCAGAGTTG 301
QY 301 ACAGTTTGAAGCTTCCCATTAAGAAATCCAGCTACTTGAATTAAGTATTCAAGTT 360
Db 302 ACAGTTTGAAGCTTCCCATTAAGAAATCCAGCTACTTGAATTAAGTATTCAAGTT 361
QY 361 AACAGAGTTTGAATATTTGATTTATCTATATATCAGTTGCAAAAGATATCTCTGCAT 420
Db 362 AACAGAGTTTGAATATTTGATTTATCTATATATCAGTTGCAAAAGATATCTCTGCAT 421
QY 421 CCTATGAGTTTCAGGCACTTATGATCTCATTAATGATTTCAAGGCCCTGCCATC 480
Db 422 CCTATGAGTTTCAGGCACTTATGATCTCATTAATGATTTCAAGGCCCTGCCATC 481
QY 481 TGTAAGGAATTTGGCACTTATCAACAAGTGAATTTCTGGATTTAGTGAAGCTG 540
Db 482 TGTAAGGAATTTGGCACTTATCAACAAGTGAATTTCTGGATTTAGTGAAGCTG 541
QY 541 CAAAATTAAGATTGCTGCAATTTGCTCACTTGAATTTCTGGATTTAGTGAAGCTG 600
Db 542 CAAAATTAAGATTGCTGCAATTTGCTCACTTGAATTTCTGGATTTAGTGAAGCTG 601
QY 601 AGAAATTTATTAATTAAGAAATGAGACAGAAAGTCAAGAAATCTGATGCAAAAAC 660
Db 602 AGAAATTTATTAATTAAGAAATGAGACAGAAAGTCAAGAAATCTGATGCAAAAAC 661
QY 661 CTTCACCTTGTGTTTCAACCAACTAGTTTATTCGCTATCCAAGTGAACATATCAGTTAT 720
Db 662 CTTCACCTTGTGTTTCAACCAACTAGTTTATTCGCTATCCAAGTGAACATATCAGTTAT 721
QY 721 ACTTTAGGCTGCTTCAACTGACTATTAATTAATGAATGATGACACTGTCAGTTTC 780
Db 722 ACTTTAGGCTGCTTCAACTGACTATTAATTAATGAATGATGACACTGTCAGTTTC 781
QY 781 ATTAATTTTATTAATGAAGTCAACAGAGTTCACCTTACGAAATTTTAACTCAACAC 840
Db 782 ATTAATTTTATTAATGAAGTCAACAGAGTTCACCTTACGAAATTTTAACTCAACAC 841
QY 841 ATAGAAAGCACTTGAAGTGCCTGCTGAGTCTTCAATTTCTTTGGCCCAACCTGTG 900
Db 842 ATAGAAAGCACTTGAAGTGCCTGCTGAGTCTTCAATTTCTTTGGCCCAACCTGTG 901
QY 901 GAATATCTCAATATTTCAATTTAACTAATATGAAAGCAATTTCTGAAAGAAATTTACT 960
Db 902 GAATATCTCAATATTTCAATTTAACTAATATGAAAGCAATTTCTGAAAGAAATTTACT 961
QY 961 TATTTTAAAGCACTTGAAGTGCCTGCTGAGTCTTCAATTTCTTTGGCCCAACCTGTG 1020
Db 962 TATTTTAAAGCACTTGAAGTGCCTGCTGAGTCTTCAATTTCTTTGGCCCAACCTGTG 1021

QY 1021 TTTTCACAGACAGCTTTGTACACCGTGTCTTGAGATGACATTATGATGTTAACATT 1080
 Db 1022 TTTTCACAGACAGCTTTGTACACCGTGTCTTGAGATGACATTATGATGTTAACATT 1081
 QY 1081 TCAGATACACCTTTTATACACATGCTGTGTCTCAATGACCAAGACATTCAGTTTGTG 1140
 Db 1082 TCAGATACACCTTTTATACACATGCTGTGTCTCAATGACCAAGACATTCAGTTTGTG 1141
 QY 1141 AACTTACCCGAAAGCTTTTCACATGATATTTTGGAAAAATGTTCCACGTTAGTTAA 1200
 Db 1142 AACTTACCCGAAAGCTTTTCACATGATATTTTGGAAAAATGTTCCACGTTAGTTAA 1201
 QY 1201 TTGGAGACCTTATCTTCAAAAAAATGATTTAAAGACCTTTTCAAGTAGTCTCAG 1260
 Db 1202 TTGGAGACCTTATCTTCAAAAAAATGATTTAAAGACCTTTTCAAGTAGTCTCAG 1261
 QY 1261 ACGAAGATATGCTCTTCTTGGAAAATCTGATGTTAGCTGGAATCTTGGAACTGTGT 1320
 Db 1262 ACGAAGATATGCTCTTCTTGGAAAATCTGATGTTAGCTGGAATCTTGGAACTGTGT 1321
 QY 1321 AGACATTAAGAAAACTGCACTGGGTGAGAGATATAGGTGTAAATTTGCTTCAAT 1380
 Db 1322 AGACATTAAGAAAACTGCACTGGGTGAGAGATATAGGTGTAAATTTGCTTCAAT 1381
 QY 1381 ATGCTTACGACTGCTGTTTTCAGATGTTTACCTCCAGAGATGAGGTACTGATCTGAC 1440
 Db 1382 ATGCTTACGACTGCTGTTTTCAGATGTTTACCTCCAGAGATGAGGTACTGATCTGAC 1441
 QY 1441 AGCAATAAATAAAGAGCGTCTCTTAACAGAGCTGTAAACCTGGAAGCTTTGGACAAGCTC 1500
 Db 1442 AGCAATAAATAAAGAGCGTCTCTTAACAGAGCTGTAAACCTGGAAGCTTTGGACAAGCTC 1501
 QY 1501 AATGTGCTTTCATCTTCTTAATCTGACCTCTTGATGTGGAGCTTTAGACGCTTTCT 1560
 Db 1502 AATGTGCTTTCATCTTCTTAATCTGACCTCTTGATGTGGAGCTTTAGACGCTTTCT 1561
 QY 1561 GTATTGATCATGATCACAATTCAGTTTCCACCCATGGGCTGATTTCTTCCAGAGCTGC 1620
 Db 1562 GTATTGATCATGATCACAATTCAGTTTCCACCCATGGGCTGATTTCTTCCAGAGCTGC 1621
 QY 1621 CAGAAGATGAGGTCAATTAAGACAGGGGACAATCCATTCATGACCTGTAGAGTAAGA 1680
 Db 1622 CAGAAGATGAGGTCAATTAAGACAGGGGACAATCCATTCATGACCTGTAGAGTAAGA 1681
 QY 1681 GAATTTGTCAAAATATAGACCAAGTATCAAGTAAAGTGTAGAGGCTGGCTGATTTCT 1740
 Db 1682 GAATTTGTCAAAATATAGACCAAGTATCAAGTAAAGTGTAGAGGCTGGCTGATTTCT 1741
 QY 1741 TATAAGTGTGACTCCCGAAGATTAATAGAGAAAGCCCACTTAAGAGACTTTTCACTGTCT 1800
 Db 1742 TATAAGTGTGACTCCCGAAGATTAATAGAGAAAGCCCACTTAAGAGACTTTTCACTGTCT 1801
 QY 1801 GAATTTATCTCTCAACATTAATCTGCTGATCGTCAACCTCGGTGCCACCATGCTGTGTG 1860
 Db 1802 GAATTTATCTCTCAACATTAATCTGCTGATCGTCAACCTCGGTGCCACCATGCTGTGTG 1861
 QY 1861 GCTGTGACTGTACCTCCCTCTGCAATCTACTGTGATCTGCTGTATCTCAGATGTGTG 1920
 Db 1862 GCTGTGACTGTACCTCCCTCTGCAATCTACTGTGATCTGCTGTATCTCAGATGTGTG 1921
 QY 1921 TGGCAGTGGACCCGAGACTCGGCGGAGAGGCCGAGAAACATACCTTAAGAAATCCAAAGA 1980
 Db 1922 TGGCAGTGGACCCGAGACTCGGCGGAGAGGCCGAGAAACATACCTTAAGAAATCCAAAGA 1981
 QY 1981 AACCTCCAGTTTCAATGCTTTTATTTATTTATATAGTGAATGATTTCTGCTGTGGTGAAGT 2040
 Db 1982 AACCTCCAGTTTCAATGCTTTTATTTATTTATATAGTGAATGATTTCTGCTGTGGTGAAGT 2041
 QY 2041 GAATTTGTAACCTTACCTGAAAAAGATATACGATTTTGTCTTACGAGAGAACTTT 2100
 Db 2042 GAATTTGTAACCTTACCTGAAAAAGATATACGATTTTGTCTTACGAGAGAACTTT 2101

QY 2101 GTCCCTGGCAGAGACATTTGGAAAAATATCATCACTGCATTTAGAGAAGTTACAAAGTCC 2160
 Db 2102 GTCCCTGGCAGAGACATTTGGAAAAATATCATCACTGCATTTAGAGAAGTTACAAAGTCC 2161
 QY 2161 ATCTTTGTTTGTCTCCCAACTTTGTCCAGAGTGTGTGCTCAATTAAGACCTTAATTT 2220
 Db 2162 ATCTTTGTTTGTCTCCCAACTTTGTCCAGAGTGTGTGCTCAATTAAGACCTTAATTT 2221
 QY 2221 GCCCATCAATCTCTTTCATGAAAGATCTAATACTTAATCTCATCTTAATGAAACC 2280
 Db 2222 GCCCATCAATCTCTTTCATGAAAGATCTAATACTTAATCTCATCTTAATGAAACC 2281
 QY 2281 ATTCACAGAAACAGATTTCCCAACAAAGTACCAAGAGCTGAAGGCTCTCATGACGAGCGG 2340
 Db 2282 ATTCACAGAAACAGATTTCCCAACAAAGTACCAAGAGCTGAAGGCTCTCATGACGAGCGG 2341
 QY 2341 ACTTATTTGCAAGTGGCCCAAGAGAAAGCAAACTGTGGCTCTTTTGGGCTTAACATTAGA 2400
 Db 2342 ACTTATTTGCAAGTGGCCCAAGAGAAAGCAAACTGTGGGCTCTTTTGGGCTTAACATTAGA 2401
 QY 2401 GCCGCTTTTAATATGAATAATTAACACTAGTCACTGAAAAACATGATGTGAATCTTAATA 2460
 Db 2402 GCCGCTTTTAATATGAATAATTAACACTAGTCACTGAAAAACATGATGTGAATCTTAATA 2461
 QY 2461 AATTAGGAAATTCACCTTAAGAAACCAATTAATTTACTTGGATGATGTGAATAGTACAGT 2520
 Db 2462 AATTAGGAAATTCACCTTAAGAAACCAATTAATTTACTTGGATGATGTGAATAGTACAGT 2521
 QY 2521 CGTAAGTAACTGTCTGAGAGTGCCTCATTTATTCCTCATAGCTTTCAGAAAGACTTAACAA 2580
 Db 2522 CGTAAGTAACTGTCTGAGAGTGCCTCATTTATTCCTCATAGCTTTCAGAAAGACTTAACAA 2581
 QY 2581 AAACAAATGTTTCATCTGGGGAACCTGAGCTAGAGCGGTGAGTTAGCTCCGCACTTGAAGAC 2640
 Db 2582 AAACAAATGTTTCATCTGGGGAACCTGAGCTAGAGCGGTGAGTTAGCTCCGCACTTGAAGAC 2641
 QY 2641 AGCCAGTCTCTGCTGGTTTATCATTAATGTTTCAATTTGAACAGCTCTTTAGTAA 2700
 Db 2642 AGCCAGTCTCTGCTGGTTTATCATTAATGTTTCAATTTGAACAGCTCTTTAGTAA 2701
 QY 2701 ATGCTCAGTTTTCAGACTCTCTCCACTCTGCTTCCCAATGATGATCTGTG 2753
 Db 2702 ATGCTCAGTTTTCAGACTCTCTCCACTCTGCTTCCCAATGATGATCTGTG 2754

RESULT 7
 AAA39809
 ID AAA39809 standard; cDNA; 2760 BP.
 XX
 AC AAA39809;
 XX
 DT 22-SEP-2000 (first entry)
 XX
 DE Human Toll-like receptor TLR6 cDNA.
 XX
 KW Toll-like receptor; TLR6; human; anti-infectious; treatment; infection;
 XX transcription factor; NF-kappaB; immune response; ss.
 OS Homo sapiens.
 FH
 FT Key Location/Qualifiers
 FT CDS 68..2458
 FT /*tag= a
 FT /product= "TLR6"
 XX
 XX WO200024776-A1.
 XX
 XX PD 04-MAY-2000.
 XX
 XX 26-OCT-1999; 99WO-JP005917.
 XX
 XX 26-OCT-1998; 98JP-00304110.
 XX

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Akira S, Takeuchi O;

XX WPI; 2000-350697/30.

DR P-PSDB; AAY8054.

XX Toll-like receptor TLR6 molecule and encoded gene, participating in
PT signal transduction of initial immune response, applicable e.g. in
PT treating infections.

XX Claim 4; Page 25-27; 35DP; Japanese.

XX This invention describes a novel toll-like receptor TLR6 which has
CC antineoplastic activity. The protein and its encoded gene have clinical
CC use e.g. in treating infections. Toll family receptors are related to
CC transcription factor NF-kappaB and regulate the expression of various
CC genes participating in the immune response. This sequence encodes the
CC human TLR6 protein which is described in the method of the invention
XX

XX Sequence 2760 BP; 850 A; 561 C; 511 G; 837 T; 0 U; 1 Other;

Query Match 99.8%; Score 2747.2; DB 3; Length 2760;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 AGAATTTGAGCTCATATCAAGATGCTCTGAAGAAGAACACCTTTAGATGACCACTGC 60
DB 2 AGAATTTGAGCTCATATCAAGATGCTCTGAAGAAGAACACCTTTAGATGACCACTGC 61
QY 61 AACATCATGACCCAAAGACAAAGAACCTTATGTTAAAGCTTCATTTGTCCTTATG 120
DB 62 AACATCATGACCCAAAGACAAAGAACCTTATGTTAAAGCTTCATTTGTCCTTATG 121
QY 121 ATCATATATGTTGGAACCAAGATCCAGTTCCTCGACGGAATGAAATTCGATGACAG 180
DB 122 ATCATATATGTTGGAACCAAGATCCAGTTCCTCGACGGAATGAAATTCGATGACAG 181
QY 181 TCAAAAAGAGGCTTATTCATTCCTCAAAAGACCTACCGCTGAAAAACCAAGCTTATGAT 240
DB 182 TCAAAAAGAGGCTTATTCATTCCTCAAAAGACCTACCGCTGAAAAACCAAGCTTATGAT 241
QY 241 ATGCTCTCAAGATTAATCGCTGAGCTTCAGGCTCTCGACATGAGCTTTCTATCAGAGTGG 300
DB 242 ATGCTCTCAAGATTAATCGCTGAGCTTCAGGCTCTCGACATGAGCTTTCTATCAGAGTGG 301
QY 301 ACAGTTTGAAGCTTTCCCAATAACAGATCCAGCTACCTTGAATTAAGTGTTCAGAGTTC 360
DB 302 ACAGTTTGAAGCTTTCCCAATAACAGATCCAGCTACCTTGAATTAAGTGTTCAGAGTTC 361
QY 361 AACCGAGATTTAGATTAATTTGATTTATCTCATTAATCACTTGCAAAAGATCTCGGCCAT 420
DB 362 AACCGAGATTTAGATTAATTTGATTTATCTCATTAATCACTTGCAAAAGATCTCGGCCAT 421
QY 421 CCTATTTGAGATTTAGATTTAGATCTCTCATTAATCACTTGCAAAAGATCTCGGCCAT 480
DB 422 CCTATTTGAGATTTAGATTTAGATCTCTCATTAATCACTTGCAAAAGATCTCGGCCAT 481
QY 481 TGTAAAGAAATTTGGCAACTTATCAACAAGTGAATTTCTTGGAGTGAAGTGAAGCTG 540
DB 482 TGTAAAGAAATTTGGCAACTTATCAACAAGTGAATTTCTTGGAGTGAAGTGAAGCTG 541
QY 541 CAAAATTTAGATTTGCTGCAATTTGCTCACTTGCATCTTAAGTTATCTTCTGAGTTTA 600
DB 542 CAAAATTTAGATTTGCTGCAATTTGCTCACTTGCATCTTAAGTTATCTTCTGAGTTTA 601
QY 601 AGAATTTATATATATAAAGAAATGAGACAGAAAGCTCAAAATTTGGAATGCAAAAAC 660
DB 602 AGAATTTATATATATAAAGAAATGAGACAGAAAGCTCAAAATTTGGAATGCAAAAAC 661
QY 661 CTTCACCTTGTGTTTTCACCAACTAGTATTTGCTATCAAGTGAACATATCAGTTAAT 720
DB 662 CTTCACCTTGTGTTTTCACCAACTAGTATTTGCTATCAAGTGAACATATCAGTTAAT 721
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QY 721 AACTTAGGGTCTTACAACTGACTAATATTAATTAATGAATGACCAACTGTCAAGTTTC 780
DB 722 AACTTAGGGTCTTACAACTGACTAATATTAATTAATGAATGACCAACTGTCAAGTTTC 781
QY 781 ATTAATTTTATATAGAACTCACAGAGGTTCAACCTTACCTGATTTTAACCTCAACAC 840
DB 782 ATTAATTTTATATAGAACTCACAGAGGTTCAACCTTACCTGATTTTAACCTCAACAC 841
QY 841 ATAGAAAGCACTTGAATGAGCTGCTGAGAGTCTTTCATTTCTTGGCCCAACCTGTG 900
DB 842 ATAGAAAGCACTTGAATGAGCTGCTGAGAGTCTTTCATTTCTTGGCCCAACCTGTG 901
QY 901 GAATATCTCAATATTTTACAAATTTTAACAATTAATGAAGCAATTCGTGAAGAAATTTACT 960
DB 902 GAATATCTCAATATTTTACAAATTTTAACAATTAATGAAGCAATTCGTGAAGAAATTTACT 961
QY 961 TATTTTAAAGACACTTGAAGAAAGCTTGAACATTAAGAACATACACAGAACCAAGTTTCTG 1020
DB 962 TATTTTAAAGACACTTGAAGAAAGCTTGAACATTAAGAACATTAAGAACCAAGTTTCTG 1021
QY 1021 TTTTCACAGACAGCTTTGTACACCGTGTGTTTCTGAGATGAACATTAATGATTAACCAAT 1080
DB 1022 TTTTCACAGACAGCTTTGTACACCGTGTGTTTCTGAGATGAACATTAATGATTAACCAAT 1081
QY 1081 TCAGATACACCTTTTATACACATGCTGTGCTCCTATGACCAAGACACATTCAGTTTTCG 1140
DB 1082 TCAGATACACCTTTTATACACATGCTGTGCTCCTATGACCAAGACACATTCAGTTTTCG 1141
QY 1141 AACTTACCACGAACGTTTTCACAGATATATTTTGAAGAAATGTTCCAGCTTATGTTAA 1200
DB 1142 AACTTACCACGAACGTTTTCACAGATATATTTTGAAGAAATGTTCCAGCTTATGTTAA 1201
QY 1201 TTGAGACACTTATCTTCAAAAAAATGATTTAAAGACCTTTTCAAGTATGATCTCATG 1260
DB 1202 TTGAGACACTTATCTTCAAAAAAATGATTTAAAGACCTTTTCAAGTATGATCTCATG 1261
QY 1261 ACGAAGATATGCTCTTCTTGGAAATATCTGATGTTAAGCTGGAATCTTGGAAATCTGCT 1320
DB 1262 ACGAAGATATGCTCTTCTTGGAAATATCTGATGTTAAGCTGGAATCTTGGAAATCTGCT 1321
QY 1321 AGACATTAAGAAACCTGCACTTGGGTTGAGATATGAGTATGATTAATTTGCTTCAAT 1380
DB 1322 AGACATTAAGAAACCTGCACTTGGGTTGAGATATGAGTATGATTAATTTGCTTCAAT 1381
QY 1381 ATGCTTACGACTGCTGTTTTCAGATGTTTACCTCCAGAGATCAAGTATGATCTTCAAC 1440
DB 1382 ATGCTTACGACTGCTGTTTTCAGATGTTTACCTCCAGAGATCAAGTATGATCTTCAAC 1441
QY 1441 AGCAATTAATAAAGAGGCTTCTTAACCAAGTCTGAATCTGAAGCTTTGCAAGAACTC 1500
DB 1442 AGCAATTAATAAAGAGGCTTCTTAACCAAGTCTGAATCTGAAGCTTTGCAAGAACTC 1501
QY 1501 AATGTTGCTTCAATCTTTTAACTGACCTTCTGAGTGTGACGACTTTAGACAGCTTTTCT 1560
DB 1502 AATGTTGCTTCAATCTTTTAACTGACCTTCTGAGTGTGACGAGCTTTTAGACAGCTTTTCT 1561
QY 1561 GTATGATCATTTGATCACAATTCAGTTTCCACCCATGCGGCTGATTTCTTCCAGAGCTGC 1620
DB 1562 GTATGATCATTTGATCACAATTCAGTTTCCACCCATGCGGCTGATTTCTTCCAGAGCTGC 1621
QY 1621 CAGAAGATGAGGTCATTAATAAGCAGGAGCAATTCATTTCAATGTACCTGTAGCTAAGA 1680
DB 1622 CAGAAGATGAGGTCATTAATAAGCAGGAGCAATTCATTTCAATGTACCTGTAGCTAAGA 1681
QY 1681 GAATTTGTCAAAAAATATAGACCAAGTATCAAGTGAAGTGTATAGAGGCTGAGCTGATCT 1740
DB 1682 GAATTTGTCAAAAAATATAGACCAAGTATCAAGTGAAGTGTATAGAGGCTGAGCTGATCT 1741
QY 1741 TATTAAGTGTACCTACCCGAAAGTATATAGAGAAACCACTTAAGAGCTTTTCAAGTGTCT 1800
DB 1742 TATTAAGTGTACCTACCCGAAAGTATATAGAGAAACCACTTAAGAGCTTTTCAAGTGTCT 1801
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QY 1801 GAATTATCCTGCAGACATTAATCTGTGATGTCACCATCGGTGCCACATGCTGTGTG 1860
DB 1802 GAATTATCCTGCAGACATTAATCTGTGATGTCACCATCGGTGCCACATGCTGTGTG 1861
QY 1861 GCTGTGACTGTGACCTCCCTCTGCACTCTTCTTGATCTTGCGCTGGTATCTCAGATGGTG 1920
DB 1862 GCTGTGACTGTGACCTCCCTCTGCACTCTTCTTGATCTTGCGCTGGTATCTCAGATGGTG 1921
QY 1921 TCCGATGGACCCAGACGTCGGGCGAGGGCGAGGAATACCCCTTAGAAGACTCCAAAAGA 1980
DB 1922 TCCGATGGACCCAGACGTCGGGCGAGGGCGAGGAATACCCCTTAGAAGACTCCAAAAGA 1981
QY 1981 AACCTCCAGTTTCATGCTTTTATTTATATAGTGAACATGATTTGCTCGGTGTAAGT 2040
DB 1982 AACCTCCAGTTTCATGCTTTTATTTATATAGTGAACATGATTTGCTCGGTGTAAGT 2041
QY 2041 GAATTGTGATCTTACTTAGAAAAAGAAATATACAGATTTGCTTCTATGAGAGAACTTT 2100
DB 2042 GAATTGTGATCTTACTTAGAAAAAGAAATATACAGATTTGCTTCTATGAGAGAACTTT 2101
QY 2101 GTCCCTGGCAAGAGATGTGAAAAATATCATCACTGATGAGAGAGTTAACAAGTCC 2160
DB 2102 GTCCCTGGCAAGAGATGTGAAAAATATCATCACTGATGAGAGAGTTAACAAGTCC 2161
QY 2161 ATCTTTGTTTGTCTCCCACTTTGTCCAGAGTGAAGTGGCCATTAAGAACTATTTT 2220
DB 2162 ATCTTTGTTTGTCTCCCACTTTGTCCAGAGTGAAGTGGCCATTAAGAACTATTTT 2221
QY 2221 GCCCATCACAATCTCTTTCATGAGAGATCTAATACTTAATCTCATCTTACTGAAACC 2280
DB 2222 GCCCATCACAATCTCTTTCATGAGAGATCTAATACTTAATCTCATCTTACTGAAACC 2281
QY 2281 ATTCACAGAAAGAGATTTCCCAACAAGTACCAACAGCTTCAATGACGACGCG 2340
DB 2282 ATTCACAGAAAGAGATTTCCCAACAAGTACCAACAGCTTCAATGACGACGCG 2341
QY 2341 ACTTATTTGCACTGGGCCCAAGAGAAACCAACAGTGGGCTCTTTGGGCTTAACATTAGA 2400
DB 2342 ACTTATTTGCACTGGGCCCAAGAGAAACCAACAGTGGGCTCTTTGGGCTTAACATTAGA 2401
QY 2401 GCCGCTTTTAAATATGAAATTAACACTAGTCACTGAAACCAATGATGTAATCTTAAGAA 2460
DB 2402 GCCGCTTTTAAATATGAAATTAACACTAGTCACTGAAACCAATGATGTAATCTTAAGAA 2461
QY 2461 AATTATGAGAAATTCACCTTAAGAAACCAATTAATTTACTTGGAGATGTAATGTAACAGT 2520
DB 2462 AATTATGAGAAATTCACCTTAAGAAACCAATTAATTTACTTGGAGATGTAATGTAACAGT 2521
QY 2521 CGTATGTAAGTGTGAGAGTGCCTTCATATCTTCATGCTCTTCAGAGAAAGACTTAACA 2580
DB 2522 CGTATGTAAGTGTGAGAGTGCCTTCATATCTTCATGCTCTTCAGAGAAAGACTTAACA 2581
QY 2581 AAAACAATGTTTCATCTGGGGAACGTGAGCTAGGCGGTGAGGTTAGCCTGCACTTAGAGAC 2640
DB 2582 AAAACAATGTTTCATCTGGGGAACGTGAGCTAGGCGGTGAGGTTAGCCTGCACTTAGAGAC 2641
QY 2641 AGCCCAAGTCTCTTCTGGTTTATCATATATGTTTCAATTTGAACAGCTCTTTTGAAGTA 2700
DB 2642 AGCCCAAGTCTCTTCTGGTTTATCATATATGTTTCAATTTGAACAGCTCTTTTGAAGTA 2701
QY 2701 ATGCTCAGTTTTCAGCTCCTCTCCAGCTGTGCTTCCCAATAGATCTGTG 2753
DB 2702 ATGCTCAGTTTTCAGCTCCTCTCCAGCTGTGCTTCCCAATAGATCTGTG 2754

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RESULT 8
ID AAS42521 standard; cDNA; 2940 BP.

XX AAS42521;

XX 18-DEC-2001 (first entry)

XX

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DE Human cDNA encoding an mdt protein, clone LI:007302.1:2000MAV01.
XX
KW Human; molecules for disease detection and treatment; mdt; ss;
KW Antiartherosclerotic; hepatotropic; antipsoriatic; cytoprotective;
KW immunosuppressive; antidiabetic; antiasthmatic; neuroprotective;
KW osteopathic; antiarthritic; cell proliferative disorder;
KW arteriosclerosis; cirrhosis; psoriasis; cancer; adenocarcinoma;
KW leukaemia; breast cancer; autoimmune disorder; AIDS;
KW acquired immunodeficiency syndrome; Addison's disease; diabetes mellitus;
KW asthma; multiple sclerosis; osteoarthritis.
XX
OS Homo sapiens.
XX
PN MO200162922-A2.
XX
PD 30-AUG-2001.
XX
PF 21-FEB-2001; 2001WO-US005896.
XX
PR 24-FEB-2000; 2000US-0185213P.
PR 16-MAY-2000; 2000US-0205232P.
PR 17-MAY-2000; 2000US-0205285P.
PR 17-MAY-2000; 2000US-0205286P.
PR 17-MAY-2000; 2000US-0205287P.
PR 17-MAY-2000; 2000US-0205323P.
PR 17-MAY-2000; 2000US-0205324P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC;
PI Chen A, D'sa SA, Amshy S, Dahl CR, Dam TC, Daniels SE, Dufour GE;
PI Flores V, Fong WT, Grenswalt LB, Hillman JL, Jones AL, Liu TF;
PI Roseberry AM, Rosen BH, Russo PD, Stocktreher TK, Daffo A;
PI Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W;
PI Cohen HU, Hodgson DM, Lincoln SE, Jackson S;
XX
DR MPI: 2001-570631/64.
XX
P-PSDB; AAN25469.
XX
PT New disease detection and treatment molecule polynucleotides and
PT polypeptides, useful for diagnosis and treatment of arteriosclerosis,
PT cirrhosis, psoriasis, cancer, autoimmune disorders, diabetes mellitus,
PT asthma and multiple sclerosis.
XX
PS Claim 1; Page 145; 183pp; English.
XX
CC The invention relates to novel human molecules for disease detection and
CC treatment (mdt proteins) and the polynucleotides encoding them. The MDT
CC polynucleotides and polypeptides are useful for diagnostic and
CC therapeutic purposes e.g. to diagnose and treat cell proliferative
CC disorders (e.g. arteriosclerosis, cirrhosis and psoriasis) cancers (e.g.
CC adenocarcinoma, leukaemia and breast cancer) autoimmune disorders (e.g.
CC acquired immunodeficiency syndrome (AIDS) and Addison's disease) diabetes
CC mellitus, asthma, multiple sclerosis, osteoarthritis, and many more
CC diseases given in the specification. The present sequence encodes an mdt
CC protein of the invention
XX
SQ Sequence 2940 BP; 896 A; 596 C; 554 G; 892 T; 0 U; 0 Other;
XX
Query Match 99.1%; Score 2727.8; DB 5; Length 2940;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2751; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
QY 1 AGAATTGGAGCTCATATCAAGTGTCTGAGAGAAACAACCCCTTAGATAGCACTGC 60
DB 2 AGAATTGGAGCTCATATCAAGTGTCTGAGAGAAACAACCCCTTAGATAGCACTGC 61
QY 61 AACATCATGACCAAGACAAAGAAACCTAATTTGTTAAACCTTCATTTGTTGCTTATG 120
DB 62 AACATCATGACCAAGACAAAGAAACCTAATTTGTTAAACCTTCATTTGTTGCTTATG 121
QY 121 ATCATTAATAGTTGGAACAGAAATCCAGTTCTCCGACGGAATGAATTTGCAGTAGACAAG 180

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Db 122 ATCATATATAGTTGGACCAAGAAATCCAGTTCTCCGACGGAAATGAATTTGGAGTAGACAAG 181
Qy 181 TCAAAAAGAGGCTTATTCATGTTCCAAAAGACCTACCGCTGAAAAACCAAGCTTAGAT 240
Db 182 TCAAAAAGAGGCTTATTCATGTTCCAAAAGACCTACCGCTGAAAAACCAAGCTTAGAT 241
Qy 241 ATGTCTCAGAACTACATCGCTGAGCTTCAGGTCCTGACATGAGCTTTCTATCAAGATTG 300
Db 242 ATGTCTCAGAACTACATCGCTGAGCTTCAGGTCCTGACATGAGCTTTCTATCAAGATTG 301
Qy 301 ACAGTTTGGAGCTTCCCATACAGAAATCCAGCTACCTGATTTAAGTGTTCAGATTTC 360
Db 302 ACAGTTTGGAGCTTCCCATACAGAAATCCAGCTACCTGATTTAAGTGTTCAGATTTC 361
Qy 361 AACCGAGATTATGAAATTTGGATTATCTCATTAATCAGTTCCAAAAGATCTCGCAT 420
Db 362 AACCGAGATTATGAAATTTGGATTATCTCATTAATCAGTTCCAAAAGATCTCGCAT 421
Qy 421 CCTATTTGAGTTTCAGGCAATTTAGATCTCTCATTCATGATTTTCAAGGCTGCCCCATC 480
Db 422 CCTATTTGAGTTTCAGGCAATTTAGATCTCTCATTCATGATTTTCAAGGCTGCCCCATC 481
Qy 481 TGTAAAGAAATTTGGCAACTTATCACAACTGAATTTCTTGGGATTTGAGTGTATGAAGCTG 541
Db 482 TGTAAAGAAATTTGGCAACTTATCACAACTGAATTTCTTGGGATTTGAGTGTATGAAGCTG 541
Qy 541 CAAAATATAGATTGCTGCAATGCTCACTTGCACTTAAGTTATATCTTCTGAGATTTA 600
Db 542 CAAAATATAGATTGCTGCAATGCTCACTTGCACTTAAGTTATATCTTCTGAGATTTA 601
Qy 601 AGAAAAT 660
Db 602 AGAAAAT 661
Qy 661 CTTCACCTGTTTTCACCCCACTGATTAATTCGCTATCCAGTGAACATACAGATTAT 720
Db 662 CTTCACCTGTTTTCACCCCACTGATTAATTCGCTATCCAGTGAACATACAGATTAT 721
Qy 721 ACTTAGAGGTGCTTACAACTGACTGATTAATTAATTAATGATGACAACTGTCAGATTTC 780
Db 722 ACTTAGAGGTGCTTACAACTGACTGATTAATTAATTAATGATGACAACTGTCAGATTTC 781
Qy 781 ATTTAAATTTTATATCAGAACTCACAGAGGTTCAACCTTACGTAATTTTACCTCAACAC 840
Db 782 ATTTAAATTTTATATCAGAACTCACAGAGGTTCAACCTTACGTAATTTTACCTCAACAC 841
Qy 841 ATGAGAAAGCACTTGGAAATGCTGCTGACAGATCTTTCATTTCTTTGGCCCAACCTGTC 900
Db 842 ATGAGAAAGCACTTGGAAATGCTGCTGACAGATCTTTCATTTCTTTGGCCCAACCTGTC 901
Qy 901 GAATATCTCAATATTTTACATTTTAACTAATTTGAAAGCACTTGTGAAAGATTTTACT 960
Db 902 GAATATCTCAATATTTTACATTTTAACTAATTTGAAAGCACTTGTGAAAGATTTTACT 961
Qy 961 TATTTTAAACGACATTTGAAGCATTTGACATATAGAACATATACAGAACCAAGTTTTCTG 1020
Db 962 TATTTTAAACGACATTTGAAGCATTTGACATATAGAACATATACAGAACCAAGTTTTCTG 1021
Qy 1021 TTTTTCACAGACGCTTTGTACACCGTGTCTTCTGAGATGACATATATATATATATATAT 1080
Db 1022 TTTTTCACAGACGCTTTGTACACCGTGTCTTCTGAGATGACATATATATATATATATAT 1081
Qy 1081 TCAGATATACCTTTTATATACAGATGCTGTGCTCATGACCAAGCACTTCAAGTTTTTG 1140
Db 1082 TCAGATATACCTTTTATATACAGATGCTGTGCTCATGACCAAGCACTTCAAGTTTTTG 1141
Qy 1141 AACTTTACCCAGAAAGTTTTTCACAGATATATTTTGAATAAAATGTTTCCAGTTAGTTAA 1200
Db 1142 AACTTTACCCAGAAAGTTTTTCACAGATATATTTTGAATAAAATGTTTCCAGTTAGTTAA 1201
Qy 1201 TTGGAGACACTTATCTTACAAAAAATGATTTAAAGACCTTTTCAAAGTAGTCTCATG 1260
Db 1202 TTGGAGACACTTATCTTACAAAAAATGATTTAAAGACCTTTTCAAAGTAGTCTCATG 1261

Qy 1261 ACGAAGATATGCTTCTTTGAAAATACATGATATGTTTACCTGAAATCTTTGAAATCTGCT 1320
Db 1262 ACGAAGATATGCTTCTTTGAAAATACATGATATGTTTACCTGAAATCTTTGAAATCTGCT 1321
Qy 1321 AGACATTAAGAAACTGCACTTTGGGTGAGAGTATAGTGTGTTTAAATTTGCTTCAAT 1380
Db 1322 AGACATTAAGAAACTGCACTTTGGGTGAGAGTATAGTGTGTTTAAATTTGCTTCAAT 1381
Qy 1381 ATGCTTACGACTCTGTTTTCAGATGTTTACCTCCAGATATCAAGTACTTATCTTAC 1440
Db 1382 ATGCTTACGACTCTGTTTTCAGATGTTTACCTCCAGATATCAAGTACTTATCTTAC 1441
Qy 1441 AGCAATTAATAAAGAGGTTCTTAAACAACTGTAATCTGAAAGCTTTGCAAGAACTC 1500
Db 1442 AGCAATTAATAAAGAGGTTCTTAAACAACTGTAATCTGAAAGCTTTGCAAGAACTC 1501
Qy 1501 AATGTTGCTTTCATATCTTTTAACTGACCTTCTGAGTGTGCACTTTAGACAGCTTCT 1560
Db 1502 AATGTTGCTTTCATATCTTTTAACTGACCTTCTGAGTGTGCACTTTAGACAGCTTCT 1561
Qy 1561 GTATTGATCATGATCACAATTCAGTTTCCCAACCATGCGCTGATTTCTCCAGAGCTGC 1620
Db 1562 GTATTGATCATGATCACAATTCAGTTTCCCAACCATGCGCTGATTTCTCCAGAGCTGC 1621
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Db 1622 CAGAAATAGAGTCAATTAAGCAAGGGGACAAATCCATTCATATGTAATCTGTGAGCTAAG 1681
Qy 1681 GAATTTGTCAAAAATATATGACCAAGTATCAAGTGAAGTGTAGAGGCTGCGCATCTCT 1740
Db 1682 GAATTTGTCAAAAATATATGACCAAGTATCAAGTGAAGTGTAGAGGCTGCGCATCTCT 1741
Qy 1741 TATATGATGACTACCCAGAAAGTATATAGAGAAAGCCCACTTAAAGAACTTTCACATGCT 1800
Db 1742 TATATGATGACTACCCAGAAAGTATATAGAGAAAGCCCACTTAAAGAACTTTCACATGCT 1801
Qy 1801 GAATTTATCTGCAACATTAATCTGCTGATCTGTCACATCTGCTGCCACATGCTGCTGTTG 1860
Db 1802 GAATTTATCTGCAACATTAATCTGCTGATCTGTCACATCTGCTGCCACATGCTGCTGTTG 1861
Qy 1861 GCTGTGACTGTGACCTTCCCTCTGCACTCTATCTTGGATCTGCTGATCTCAGATGCTG 1920
Db 1862 GCTGTGACTGTGACCTTCCCTCTGCACTCTATCTTGGATCTGCTGATCTCAGATGCTG 1921
Qy 1921 TGCCAGTGAAGCCAGACTCGGGGACAGGGCCAGAAACATACCTTGAAGAACTCCAAAGA 1980
Db 1922 TGCCAGTGAAGCCAGACTCGGGGACAGGGCCAGAAACATACCTTGAAGAACTCCAAAGA 1981
Qy 1981 AACCTCAGATTTCATGCTTTTATTTTATATATATATATATATATATATATATATATAT 2040
Db 1982 AACCTCAGATTTCATGCTTTTATTTTATATATATATATATATATATATATATATATAT 2041
Qy 2041 GAATTTGTATCTTACCTTACGAAAGAAAGATATATACATTTTGTCTTATGAGAGAACTTT 2100
Db 2042 GAATTTGTATCTTACCTTACGAAAGAAAGATATATACATTTTGTCTTATGAGAGAACTTT 2101
Qy 2101 GTCCCTGCAAGAGATTTGGAATAATATATATATATATATATATATATATATATATAT 2160
Db 2102 GTCCCTGCAAGAGATTTGGAATAATATATATATATATATATATATATATATATATATAT 2161
Qy 2161 ATCTTTGTTTGTCTCCCAACTTTTGTCCAGAGTGAAGTGTGCTATTCAGAACTATATTT 2220
Db 2162 ATCTTTGTTTGTCTCCCAACTTTTGTCCAGAGTGAAGTGTGCTATTCAGAACTATATTT 2221
Qy 2221 GCCCATCAATCTCTTTCATGAGAGATCTAATACTTAATCTTCATCTTACCTGAAACC 2280
Db 2222 GCCCATCAATCTCTTTCATGAGAGATCTAATACTTAATCTTCATCTTACCTGAAACC 2281
Qy 2281 ATTCACAGAACAGATTTCCCAACAAAGTACCAAGAGGCTCTCATGACGAGCGG 2340
Db 2282 ATTCACAGAACAGATTTCCCAACAAAGTACCAAGAGGCTCTCATGACGAGCGG 2341

QY 2341 ACTATTTCAGTGGCCCAAGAGAAACAAACGT -GGGCTCTTTTGGGCTAACATTAG 2399
XX |||||
Db 2342 ACTATTTCAGTGGCCCAAGAGAAACAAACGTGGGGCTCTTTGGGCTAACATTAG 2401
QY 2400 ACCCGCTTTTAATATGAATTAACACTAGTCACTGAAAAACATGATGTGAATCTTAAAA 2459
Db 2402 ACCCGCTTTTAATATGAATTAACACTAGTCACTGAAAAACATGATGTGAATCTTAAAA 2461
QY 2460 AAATTAGGAATTCAACTTAAGAAACCAATTATTTCTTGGATGATGGTAATAGTACAG 2519
Db 2462 AAATTAGGAATTCAACTTAAGAAACCAATTATTTCTTGGATGATGGTAATAGTACAG 2521
QY 2520 TCGTAAGTAACTGTCTGAGAGTGCCCTCCATTATCTCATGCTTCAGAAAAAGCTTAACA 2579
Db 2522 TCGTAAGTAACTGTCTGAGAGTGCCCTCCATTATCTCATGCTTCAGAAAAAGCTTAACA 2581
QY 2580 AAAACAAATTTTCATCTGGGGAACTGAGCTAAGCGGTGAGTTAGCTGCCAGTTAGAGA 2639
Db 2582 AAAACAAATTTTCATCTGGGGAACTGAGCTAAGCGGTGAGTTAGCTGCCAGTTAGAGA 2641
QY 2640 CAGCCAGCTCTCTGCTGTTAATCATTTATGTTTCAATT -GAAACAGTCTCTTTGAGT 2698
Db 2642 CAGCCAGCTCTCTGCTGTTAATCATTTATGTTTCAAAATGGAAACAGTCTCTTTGAGT 2701
QY 2699 AAATCTCAGTTTTCAGCTCCTCTCCACTCTGCTTCCCAATGATCTGTG 2753
Db 2702 AAATCTCAGTTTTCAGCTCCTCTCCACTCTGCTTCCCAATGATCTGTG 2756
RESULT 9
ADVA42616
ID ADVA42616 standard; cDNA; 2391 BP.
XX
AC ADVA42616;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human psychoneuroendocrine immune expressed sequence tag SEQ ID NO 244.
XX
KW microarray; psychoneuroendocrine immune; chronic fatigue;
KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
EN WO2004108899-A2.
XX
PD 16-DEC-2004.
XX
PF 04-JUN-2004; 2004MO-US017686.
XX
PR 04-JUN-2003; 2003US-0475915P.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Nicholson A, Vernon SD;
XX
XX WPI; 2005-031682/03.
XX
XX New microarray comprising probes for genes involved in
XX psychoneuroendocrine immune (PNI) activity, useful in diagnosing a
XX PT condition associated with PNI activity, e.g., inflammatory or infectious
XX PT diseases.
XX
XX Claim 1; SEQ ID NO 244; 254bp; English.
XX
XX The invention relates to a new microarray which comprises probes for
XX CC genes involved in psychoneuroendocrine immune (PNI) activity. The
XX CC microarray is useful in diagnosing a condition associated with PNI
XX CC activity, such as CRS, type-2 diabetes, allergic condition, inflammation,
XX CC cancer and infection. The present sequence represents a
XX CC psychoneuroendocrine immune gene expressed sequence tag. Note the
XX CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to

CC SEQ ID NO 1829 are provided.
XX
SQ Sequence 2391 BP; 742 A; 485 C; 436 G; 728 T; 0 U; 0 Other;
Query Match 86.9%; Score 2391; DB 14; Length 2391;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 67 ATGACCAAGACAAAGAACCTATTGTTAAACCTTCATTTGCTTATGATGATCA 126
Db 1 ATGACCAAGACAAAGAACCTATTGTTAAACCTTCATTTGCTTATGATGATCA 60
QY 127 ATAGTTGGAACCAAGATCCAGTTCTCCAGCGAAATGAATTTGAGTAGACAAGTCAAA 186
Db 61 ATAGTTGGAACCAAGATCCAGTTCTCCAGCGAAATGAATTTGAGTAGACAAGTCAAA 120
QY 187 AGAGGCTTATTCATGTTCCAAAGACCTACCGCTGAAAAACCAAGTCTTAGATATGCT 246
Db 121 AGAGGCTTATTCATGTTCCAAAGACCTACCGCTGAAAAACCAAGTCTTAGATATGCT 180
QY 247 CAGAACTACATGCTGAGGCTTCAAGGCTCTGACATGAGGCTTCTATCAGAGTTGACATT 306
Db 181 CAGAACTACATGCTGAGGCTTCAAGGCTCTGACATGAGGCTTCTATCAGAGTTGACATT 240
QY 307 TTGAGACTTCCCATTAACGAATCCAGCTACTGATTATTAAGTGTTCGAAGTTCAACGAG 366
Db 241 TTGAGACTTCCCATTAACGAATCCAGCTACTGATTATTAAGTGTTCGAAGTTCAACGAG 300
QY 367 GATTTAGAAATATTTGATTTATCTCATATATCAGTTGCAAAAGATATCTGCATCTATT 426
Db 301 GATTTAGAAATATTTGATTTATCTCATATATCAGTTGCAAAAGATATCTGCATCTATT 360
QY 427 GTGAGTTTCAGGCAATTTAGATCTCTCATTCATGATTTTCAAGCCCTGCTGATG 486
Db 361 GTGAGTTTCAGGCAATTTAGATCTCTCATTCATGATTTTCAAGCCCTGCTGATG 420
QY 487 GAATTTGGCAACTTATCACTCAACTGAATTTCTGGGATGAGTGTATGAGGTGCAAAAA 546
Db 421 GAATTTGGCAACTTATCACTCAACTGAATTTCTGGGATGAGTGTATGAGGTGCAAAAA 480
QY 547 TTGAGTTTGTGCGCAATTTGCTCACTTGCATCTGATGATGATATCTTGTGATTTAAGAAAT 606
Db 481 TTGAGTTTGTGCGCAATTTGCTCACTTGCATCTGATGATGATATCTTGTGATTTAAGAAAT 540
QY 607 TATTTATATTAAGAAATGAGACAGAAAGTCTACAAATTTGCAATGCAAAAAACCTTCAAC 666
Db 541 TATTTATATTAAGAAATGAGACAGAAAGTCTACAAATTTGCAATGCAAAAAACCTTCAAC 600
QY 667 CTGTTTTCACCCCAACTAGTTTATTTGGCTATCCAAAGGAACATATCAGTTAATCTTTA 726
Db 601 CTGTTTTCACCCCAACTAGTTTATTTGGCTATCCAAAGGAACATATCAGTTAATCTTTA 660
QY 727 GGGTGCTTACAACTGACTTAATTAATTTGAATGATGACAACTGCAAGTTTTCATTAAA 786
Db 661 GGGTGCTTACAACTGACTTAATTAATTTGAATGATGACAACTGCAAGTTTTCATTAAA 720
QY 787 TTTTATATGAAACTACACAGAGTTCAACTTACTGAATTTTACCTTCAACCACTAGAA 846
Db 721 TTTTATATGAAACTACACAGAGTTCAACTTACTGAATTTTACCTTCAACCACTAGAA 780
QY 847 ACGACTTGAATATGCTGCTGAGAGTCTTTCAATTTCTTGGCCCAACCTGTGGAATAT 906
Db 781 ACGACTTGAATATGCTGCTGAGAGTCTTTCAATTTCTTGGCCCAACCTGTGGAATAT 840
QY 907 CTCATATTTTCAATTTAACAATTAATTTGAAGCATTCGTGAAGAAATTTTACTATTCT 966
Db 841 CTCATATTTTCAATTTAACAATTAATTTGAAGCATTCGTGAAGAAATTTTACTATTCT 900
QY 967 AAAAGCAATTTGAAGATTTGACATATGACATATACAGAACCAAGTTTCTGTGTTTCA 1026
Db 901 AAAAGCAATTTGAAGATTTGACATATGACATATACAGAACCAAGTTTCTGTGTTTCA 960
QY 1027 CAGACAGCTTGTACACCGTGTGTTTCTGAGATGAACATTAATGATGTAAACATTTCAAT 1086

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Db      ||| 961 CAGACAGCTTGTGTACACCGTGTCTTCTGAGATGAACATATGATGATTAACCATTTCAAGT 1020
Qy      ||| 1087 ACACCTTTTATACACATGCTGTGCTCTCATGCAACAGACATTAAGTTTGAACCTT 1146
Db      ||| 1021 ACACCTTTTATACACATGCTGTGCTCTCATGCAACAGACATTAAGTTTGAACCTT 1080
Qy      ||| 1147 ACCGAAACGTTTTCACAGATAGTATTTTGGAAAAATGTTCCACGTTAGTTAAATTTGAG 1206
Db      ||| 1081 ACCGAAACGTTTTCACAGATAGTATTTTGGAAAAATGTTCCACGTTAGTTAAATTTGAG 1140
Qy      ||| 1207 ACACCTTATCTTACAAAAATGATTAAGACCTTTTCAAGTATGCTTCAATATGCTT 1266
Db      ||| 1141 ACACCTTATCTTACAAAAATGATTAAGACCTTTTCAAGTATGCTTCAATATGCTT 1200
Qy      ||| 1287 GATATGCTCTCTTGGAAAAATATGATATGTTAGCTGGAATCTTTGGAATCTGCTGACAT 1326
Db      ||| 1201 GATATGCTCTCTTGGAAAAATATGATATGTTAGCTGGAATCTTTGGAATCTGCTGACAT 1260
Qy      ||| 1327 AAAGAAACCTGACCTTGGGTTGAGATATAGTGTGTTAAATTTGCTTCAATATGCTT 1386
Db      ||| 1281 AAAGAAACCTGACCTTGGGTTGAGATATAGTGTGTTAAATTTGCTTCAATATGCTT 1320
Qy      ||| 1387 ACTGACTCTGTTTTCAGATGTTTAACTCCAGATCAAGGTACTTGATTTTCAACGCAAT 1446
Db      ||| 1321 ACTGACTCTGTTTTCAGATGTTTAACTCCAGATCAAGGTACTTGATTTTCAACGCAAT 1380
Qy      ||| 1447 AAAATAAAGAGCGTTCCTAAACAAGTCGTAACCTGGAAAGCTTTCGAAACATCAATGTT 1506
Db      ||| 1381 AAAATAAAGAGCGTTCCTAAACAAGTCGTAACCTGGAAAGCTTTCGAAACATCAATGTT 1440
Qy      ||| 1507 GCTTTCATTTCTTAACTGACCTTCTCGATGTGGAGCTTTAGACGCTTTCTGTATTTG 1566
Db      ||| 1441 GCTTTCATTTCTTAACTGACCTTCTCGATGTGGAGCTTTAGACGCTTTCTGTATTTG 1500
Qy      ||| 1567 ATCATTGATCACAATTCAGTTTCCACCCATGCGCTGATTTCTTCCAGAGCTGCCAAG 1626
Db      ||| 1501 ATCATTGATCACAATTCAGTTTCCACCCATGCGCTGATTTCTTCCAGAGCTGCCAAG 1560
Qy      ||| 1627 ATGAGGTCAATTAAGACGAGGGGACAAATCCATTCOAATGTAACCTGAGAGTAAGAAATTT 1686
Db      ||| 1561 ATGAGGTCAATTAAGACGAGGGGACAAATCCATTCOAATGTAACCTGAGAGTAAGAAATTT 1620
Qy      ||| 1687 GTCAAAAATATAGACCAAGTATCAAGTGAAGTGTATAGAGGGCTGGCTGATTTCTTAAAG 1746
Db      ||| 1621 GTCAAAAATATAGACCAAGTATCAAGTGAAGTGTATAGAGGGCTGGCTGATTTCTTAAAG 1680
Qy      ||| 1747 TGTGACTACCCAGAAAGTTATAGAGAGCCCACTAAGAGACTTTTCAATGTTCTGAATTA 1806
Db      ||| 1681 TGTGACTACCCAGAAAGTTATAGAGAGCCCACTAAGAGACTTTTCAATGTTCTGAATTA 1740
Qy      ||| 1807 TCCCTGCAACATTAACCTGCTGATGCTGACATGCGGGGACCAATGCTGCTGTGCTG 1866
Db      ||| 1741 TCCCTGCAACATTAACCTGCTGATGCTGACATGCGGGGACCAATGCTGCTGTGCTG 1800
Qy      ||| 1867 ACTGTGACCTCCCTCTGACATCTACTTGTGATCTGCTGCTGATCTCAGATGCTGCTCAG 1926
Db      ||| 1801 ACTGTGACCTCCCTCTGACATCTACTTGTGATCTGCTGCTGATCTCAGATGCTGCTCAG 1860
Qy      ||| 1927 TGGACCCAGACTGCGGGCGAGGGCGAGGAACATACCTTTAGAAAGACTCCAAAGAAACCTC 1986
Db      ||| 1861 TGGACCCAGACTGCGGGCGAGGGCGAGGAACATACCTTTAGAAAGACTCCAAAGAAACCTC 1920
Qy      ||| 1987 CAGTTTCATGCTTTTATTTTATATAGTGAACATGATTCGGCTGGGTTGAAAAAGTGAATTG 2046
Db      ||| 1921 CAGTTTCATGCTTTTATTTTATATAGTGAACATGATTCGGCTGGGTTGAAAAAGTGAATTG 1980
Qy      ||| 2047 GTACCTTACCTAGAAAAAGAGATATACAGATTTGTCTTATGAGAGAACTTTGTCCCT 2106
Db      ||| 1981 GTACCTTACCTAGAAAAAGAGATATACAGATTTGTCTTATGAGAGAACTTTGTCCCT 2040
Qy      ||| 2107 GGCAGAGCATTGTGAAAAATATCATCAACTGCAATTGAGAGAGTTTCAAGTCCATCTTT 2166

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Db      2041 GGCAGAGCATTGTGAAAAATATCATCACTGCAATTGAGAAAGTTACAGTCCATCTTT 2100
Qy      2167 GTTTTGTCTCCCAACTTTGTCTCAGAGTGAAGTGTCCTATTAAGAACTCTATTTGGCCAT 2226
Db      2101 GTTTTGTCTCCCAACTTTGTCTCAGAGTGAAGTGTCCTATTAAGAACTCTATTTGGCCAT 2160
Qy      2227 CACAACTCTCTTTCATGAAGAGTCTPAATACCTTAATCTCTATCTTACTGGAACCCATTTCCA 2286
Db      2161 CACAACTCTCTTTCATGAAGAGTCTPAATACCTTAATCTCTATCTTACTGGAACCCATTTCCA 2220
Qy      2287 CAGAACACATTTCCCAACAAATACCAAGCTGAAGGCTCCATGAGACGACGAGCACTTAT 2346
Db      2221 CAGAACACATTTCCCAACAAATACCAAGCTGAAGGCTCCATGAGACGACGAGCACTTAT 2280
Qy      2347 TTGCACTGCCCCAAGAGAAAGCAACGTTGGGCTCTTTTGGGCTPAACATTAGACCGCT 2406
Db      2281 TTGCACTGCCCCAAGAGAAAGCAACGTTGGGCTCTTTTGGGCTPAACATTAGACCGCT 2340
Qy      2407 TTTAATATGAATTAACACTAGTCACTGAAAAACAATGATGTGAAATCTTAA 2457
Db      2341 TTTAATATGAATTAACACTAGTCACTGAAAAACAATGATGTGAAATCTTAA 2391

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RESULT 10

AAA39810
ID AAA39810 standard; cDNA; 2604 BP.

XX AAA39810;

AC 22-SEP-2000 (first entry)

XX 22-SEP-2000 (first entry)

XX Murine Toll-like receptor TLR6 cDNA.

XX Toll-like receptor; TLR6; murine; anti-infectious; treatment; infection;

XX transcription factor; NF-kappaB; immune response; ss.

XX Mus sp.

OS Mus sp.

XX Key Location/Qualifiers

XX CDS 21..2442

XX FT /tag=a

XX FT /product="TLR6"

XX WO200024776-A1.

XX PD 04-MAY-2000.

XX PF 26-OCT-1999; 99WO-JP005917.

XX PR 26-OCT-1998; 98JP-00304110.

XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX PI Akira S, Takeuchi O;

XX DR WPI; 2000-350697/30.

XX DR P-PSDB; AAY88055.

XX PT Toll-like receptor TLR6 molecule and encoded gene, participating in

XX PT signal transduction of initial immune response, applicable e.g. in

XX PT treating infections.

XX PS Claim 4; Page 29-30; 35pp; Japanese.

This invention describes a novel toll-like receptor TLR6 which has anti-infectious activity. The protein and its encoded gene have clinical use e.g. in treating infections. Toll family receptors are related to transcription factor NF-kappaB and regulate the expression of various genes participating in the immune response. This sequence encodes the murine TLR6 protein which is described in the method of the invention

Sequence 2604 BP; 689 A; 615 C; 561 G; 739 T; 0 U; 0 Other;

Query Match 55.7%; Score 1533.6; DB 3; Length 2604;
Best Local Similarity 76.1%; Pred. No. 0;
Matches 1930; Conservative 0; Mismatches 596; Indels 10; Gaps 3;

QY 17 TCAAGATGCTCGAAGAAACAACCCCTTGAAGTACCACTGCAACATCATGACCAAG 76
DB 4 TAAAAATGCTGAGAAATGTAATGTCCTCTGGAGTAGCCTCTGCAACATGAGCAAG 63

QY 77 ACAAAAGACCTATGTTAAAGCTTCATTTTGTTCCTATGATCATATATGTTGAA 136
DB 64 ACGAAAGACCCATCGTGGGAGTTTCACCTTGTTCGCGCTGACCTTAATATGTGGA 123

QY 137 CCGAATCCAGTCTCTCGACGGAATGAATTTGACATAGCAAGTCAAAAGAGCTTGA 196
DB 124 GATAGACCCCGTCTCTATATGAATTTGAGTCTATGATAGTCTTCAAAAGAACCTTA 183

QY 197 TTCTATGTTCCAAAAGACCTACCGCTGAAAAACAAGCTTATATGTCAGAACTACA 256
DB 184 CTCATGTCCCAAGACCTGCCCAAGAAACAAAGCCCTGAGTCTGTCTCAAAACTCTA 243

QY 257 TCGCTGAGCTTCAAGTCTCTGACATAGAGCTTCTATCAGAGTTGACAGTTTGA 316
DB 244 TATCTGAGCTTGGAGCTCTGATATCAGCTTCTGTGAGAGCTGAGAGTTCTGA 303

QY 317 CCCATPACAGAAATCCAGTACTGATTTTAAAGTTCCTTCAAGTTCAACGAGATTTGAAT 376
DB 304 CCCAACAGAGATCGGAGCCTTGAATTTTCATGATTTCTTGTTCATTCAGAGCTTGAAT 363

QY 377 ATTTGATTTATCTCATTAATCAAGTTGCAAAAGATATCTGCCATCTTATGTAAGTTGA 436
DB 364 ACCTGATGTCTACACATCGGTTGCAAAACATCTTGTGCGCCCTATGGGAGCTGA 423

QY 437 GGCATTTAGATCTCTCATTCATGATTTCAAGGCCCTGCCATCTTGAAGAAATTTGGA 496
DB 424 GGCATCTACACCTCATCAATGATTTGATGTACTGCTGTGTGAAGAAATTTGGA 483

QY 497 ACTTATCAACATGSAATTTCTGGAGTTGAGTCTAAGAGCTGCAAAATATGATTTGC 556
DB 484 ACTGACAGAGCTGACTTCTGTGAGTAAGTGTGCTGCAAGTTCCGACAACTGAGTCTGC 543

QY 557 TGCATATGCTCATCTTCAATGATTTATATCTTCTGATTTTAAAGAAATTTATATATA 616
DB 544 TCCAGTGTCTCATCTTGAATGATGATCTTCTGACCTTGAAGTCAATCATATATA 603

QY 617 AAGAAATGAGCAGAAAGTCTTCAATTTCTGAATGCAAAACCTTCACTTGTTC 676
DB 604 AAGGCGGGAAACAGAAAGTCTTCAATTTCCCAATCCACCGTCTCCATTTGTTC 663

QY 677 ACCCACTAGTTTATGCTATCAAGTACATATCAGTTAATCTTAAAGGTGCTTAC 736
DB 664 ATCCAAATAGCTTGTCTGTGTAAGTAACATGTCTGTAACGCTTTAAGACATTTAC 723

QY 737 AACTGACTATATTAATTAATGAATGATGACACTGTCAAGTTTTCATTAATTTTATACG 796
DB 724 AACTAGATATATTAATTAATGAATGAAACTGTCAAGGTTAATGACATTTTATACG 783

QY 797 AACTACACGAGGTTCAACCTTACTGAATTTTACCTCAACACATAGAAAGCACTTGA 856
DB 784 AACTACACGAGGTTCAACCTTACTGAATTTTACCTCAACACATAGAAAGCACTTGA 843

QY 857 AATGCTGGTCAAGCTTCTCAATTTCTTGGCCCAACCTGGAATCTCAATATTT 916
DB 844 AATGCTGGTCAAGCTTCTCAATTTCTTGGCCCAACCTGGAATCTCAATATTT 903

QY 917 ACAATTTAACAATTAATGAAGCATTCGTGAAGAAAGATTTTACTTATTTAAACGACAT 976
DB 904 ACAATTTAACAATTAATGAAGCATTCGTGAAGAAAGATTTTACTTATCTGAGAGACGAC 963

QY 977 TGAAGAGATGACATGATGACATATCAGAACCAAGTTTCTGTTCACGACAGCTT 1036
DB 964 TGAAGAGATGATGATGACAGCTTCAAAAACCAAGTGTTCCTTTTAAAGAGGCGC 1023

QY 1037 TGTACACGCTGTTTCTGATGAAACATATGATGTTAACATTTACATACCTTTTA 1096

DB 1024 TATACCTGGTGTGTTGCTGATGAGACATCAAGATGCTCTATCTCAGACACCCCTTCA 1083
QY 1097 TACACATGCTGTGTCTCATGACCAAGACATTCAGATTTTGAACCTTACCAGACG 1156
DB 1084 TCCACATGCTGTGTGCGGCATCCCAAGCTCATTTTCAATTTGAACTTTACCCAGAAAG 1143

QY 1157 TTTTACAGATATGTAATTTTGAAGAAATGTTCCACGTAATTAATTTGAGACATTAATCT 1216
DB 1144 TTTTATCTACAGTGTGTTTCAAGGCTGTTCACCTTAAAGATTTGACACATTAATCT 1203

QY 1217 TACAAAAATATGATTTAAAGACCTTTTCAAGTATGCTCATGACGAAGATATGCTT 1276
DB 1204 TACAAAGATGTTGTAAGAACTTTTAAAGTATGCTCATGACTAAGAAATATGCTCT 1263

QY 1277 CTTTGAATTAAGTATGTTAGCTGAATCTTTTGAATCTGTGATGACATAAAGAACT 1336
DB 1264 CTCTGGAACCTTTGATGTTAGTTGAATTTCTTGAACCTCATGACATGACAGACAT 1323

QY 1337 GCACTTTGGTGAAGTATAGTGTCTTAATTTGTCTTCAATATGCTTACTGACTTG 1396
DB 1324 GCGCTGGGCTGAGACATATGTTGTAATTTGTCTGCAATATGTTACAGGCTCTG 1383

QY 1397 TTTTCAAGTGTTAACCTCCAGGATCAAGGTAATGATCTTCAACAGCAATTAATAA 1456
DB 1384 TCTTCAAGTGTTAACCTCCAGGATCAAGGTAATGATCTTCAACAGCAATTAATAA 1443

QY 1457 GCGTCTTAACAGATGTTAAAGCTGGAAGCTTTGCAAGAACTCAATGTTGCTTCAAT 1516
DB 1444 GCATCCCTTAAGATGTTCAACCACTGACAGGCTTTGCAAGAACTCAATGTTGCTTCAAT 1503

QY 1517 CTTTAACTGACCTTCTGATGATGTCAGCTTTAGACGCTTCTGATTTGATGATTTGATC 1576
DB 1504 CTTTAACTGACCTTCTGATGATGTCAGGCTTTGATGATGATGATGATGATGATGATC 1563

QY 1577 ACAATTCAGTTTCCCAACCATCGGCTGATTTCTTCAAGAGCTGCCAGAAATGAGGTCA 1636
DB 1564 ATTAATCTGATTTCCCATCTCTGAGATTTCTTCAAGAGCTGCCAGAAATGAGGTCA 1623

QY 1637 TAAAAAGAGGAGCAATCCATTCATGATGATGATGATGATGATGATGATGATGATGAT 1696
DB 1624 TAAAGAGGAGAAACAACCATTCATGATGATGATGATGATGATGATGATGATGATGAT 1683

QY 1697 TAGACCAAGTATCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1756
DB 1684 TAGGCTGGGTGCAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1743

QY 1757 CAGAAATTAATGAGAAAGCCCACTAAAGGACTTTCACATGCTGAATTAATCTGCAACA 1816
DB 1744 CAGAAAGCTTAAGGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1803

QY 1817 TAATCTGTGATGTCATCCATCGATGTCACCATGTCGATGTCGATGTCGATGTCGATGTC 1876
DB 1804 CTGTTCTGTGATGTCATCCATCGATGTCACCATGTCGATGTCGATGTCGATGTCGATGTC 1863

QY 1877 CCTTGTGATCTTACTTGTGATCTGCTGTGATCTCAAGATGTCGATGTCGATGTCGATGTC 1936
DB 1864 TCCCTGTGATCTTACTTGTGATCTGCTGTGATCTCAAGATGTCGATGTCGATGTCGATGTC 1923

QY 1937 CTGGGCGAGGCGCAGAAACATACCTTGAAGAACTCCAAAGAAAGCTCCAGTTTCAAG 1996
DB 1924 CCGAGCAGAGGCGCAGGACATCCCTTGAAGAACTCCAAAGAAAGCTCCAGTTTCAAG 1983

QY 1997 CTTTATTTTCAATATGTAACATGATGTCCTGCTGGGTGAAGATGATGATGATGATGATGAT 2056
DB 1984 CTTTGTCTCATATCAGTGAAGATGATGTCCTGCTGGGTGAAGATGATGATGATGATGATGAT 2043

QY 2057 TAGAAAGAGATATTAAGATTTGCTTCAATGAAAGAACTTGTCTCTGCAAGACCA 2116
DB 2044 TAGAAAGAGATATTAAGATTTGCTTCAATGAAAGAACTTGTCTCTGCAAGACCA 2103

QY 2117 TTGTGAAATATATCATCAATGATGAAAGATTAAGAGTCAATCTTGTGTTGTCTC 2176

QY 977 TGAAGCATTTGACAAATAGACATATCATCGAACCAAGTTTTCTGTTTTCACAGACGCTT 1036
 Db 964 TGAAGCATTTGACAAATAGACATATCATCGAACCAAGTTTTCTGTTTTCACAGACGCTT 1023
 QY 1037 TGTACACCGTGTGTTTCTGAGTAGAAGACATTATGTTAAACATTTCAGATPACACTTTTA 1096
 Db 1024 TATACTCGGTGTTTGTGTGATGAAACATCAAGTGTCTCTATCTCAGACACCCCTTTCA 1083
 QY 1097 TACACATGCTGTGCTCATGACCAAGACATTTCAAGTTTTGAACTTTACCCAGAAG 1156
 Db 1084 TCCACATGCTGTGCTCATGACCAAGCTCCAGCTCATTTACATTCTGAACTTTACCCAGAAG 1143
 QY 1157 TTTTCACAGATAGTATTTTGAAGAAATGTTCCACGTTAGTAAATTTGAGACACTTATCT 1216
 Db 1144 TTTTACTGACAGTGTGTTTTCAGAGCTGTTCCACTTAAGAGATTGACAGACACTTATCT 1203
 QY 1217 TACAAAAAATGATTTAAAGACCTTTTCAAGTAGTCTCATGACGAAGATATGCTT 1276
 Db 1204 TACAAAGGATGTTGAAGAACTTTTAAAGTAGCTCATGACTAAGAAATATGCTT 1263
 QY 1277 CTTTGGAAATATGATGTTAGTCTGGAATCTTTGGAATCTGTGATGACATTAAGAAACT 1336
 Db 1264 CTTGGAATCTTTGATGTTGATTTGAAATCTTGAATCTCATGATATGACAGACAT 1323
 QY 1337 GCACTTGGGTGAGATATAGTGTGTTAAATTTGCTTCAATATGCTTACGACTCTG 1396
 Db 1324 GGGCTTGGGTGAGACATATGTTGTTGAAATTTGCTTCAATATGCTTACGACTCTG 1383
 QY 1397 TTTTCAGATGTTTACCTCCAGAGATCAAGTATCTTGATCTTCAAGCAATTAATTAAGA 1456
 Db 1384 TCTTCAGATGTTTACCTCCAGAGATCAAGTATCTTGATCTTCAAGCAATTAATTAAGA 1443
 QY 1457 GCGTTCCTAAACATTCGTAACCTGGAAGCTTTGCAAGACTCAATGTTGCTTCAAT 1516
 Db 1444 GCATCCCTAAAGATGTCAACCCACCTGACAGCTTTGCAAGACTCAATGATGATCCACT 1503
 QY 1517 CTTTACTGACCTTCTGATGTTGACGAGCTTTAGACGCTTCTGATGATCATTTGATC 1576
 Db 1504 CTTTACTGACCTTCTGATGTTGACGAGCTTTAGACGCTTCTGATGATCATTTGATC 1563
 QY 1577 ACAATTCAGTTTCCACCCATGAGCTGATTTCTTCCAGACCTGCAAGAGATGAGTCA 1636
 Db 1564 ATAATCTAGTTTCCATCCCTGAGGATTTCTTCCAGACCTGCAAGATTAATGATCC 1623
 QY 1637 TAAAGCGGAGACATTCATTCATGATGATGATGATGATGATGATGATGATGATGAT 1696
 Db 1624 TAAAGCGGAGACATTCATTCATGATGATGATGATGATGATGATGATGATGATGAT 1683
 QY 1697 TAGACCAAGTATCAAGTGAAGTGAAGGCTGAGCTGATCTTATAAGTGAATACC 1756
 Db 1684 TAGGCTGGGTGCAAGAGAGAGGCTGAGGCTGAGCTGATCTTATAAGTGAATACC 1743
 QY 1757 CAGAAAGTTATAGAGAGACCCATTAAGAACTTTCAACATGCTGAATATCTGCAACA 1816
 Db 1744 CAGAAAGTTATAGAGAGACCCATTAAGAACTTTCAACATGCTGAATATCTGCAACA 1803
 QY 1817 TAACTGTGATGCTCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 1876
 Db 1804 CTGTTCTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1863
 QY 1877 CCGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1936
 Db 1864 TCTCTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1923
 QY 1937 CTCGGCAGAGCCAGAAATATCCCTTAAGAACTTCCAAAGAACTCCAGTTTCAATG 1996
 Db 1924 CCAGCACAAGGCGCAGGACATCCCTTAAGAACTTCCAAAGAACTCCAGTTTCAATG 1983
 QY 1997 CTTTATTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2056
 Db 1984 CTTTGTCTCATACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2043
 QY 2057 TAGAAAAAGATATACGATTTGCTTTCATGAGAGAACTTTGCTCCGCAAGAGA 2116

Db 2044 TAGAGAAAGATGACATCCGAGTTGCTTCATGAGAGAACTTTGCTCCGCAAGAGA 2103
 QY 2117 TGTGAAAAATATCATCACTGATGAGAGAGTTACAAAGTCAATCTTTGTTGCTTC 2176
 Db 2104 TGTGAGAAATATCATCACTGATGAGAGAGTTACAAAGTCAATCTTTGTTGCTTC 2163
 QY 2177 CCAACTGTTCCAGAGTGAAGTGCATTAAGAACTGATTTGTCATCAATCTCT 2236
 Db 2164 CCAACTGTTCCAGAGTGAAGTGCATTAAGAACTGATTTGTCATCAATCTCT 2223
 QY 2237 TTTCAAGAGATCTAATACTTAATCTCATCTTAAGAACTTCCAGAAACAGCA 2296
 Db 2224 TCCATGAAGGCTCTGATTAATCTCATCTTCTGAGAACTTCCAGAAACAGCA 2283
 QY 2297 TTTCCAAAGATGACCAAGGCTCTGATGAGAGGAGCTTAATTTGCACTGCTC 2356
 Db 2284 TTTCCAAAGATGACCAAGGCTCTGATGAGAGGAGCTTAATTTGCACTGCTC 2343
 QY 2357 CCAAGGAGAAAGCAAGTGGGCTTTTGGGCTTAACATTAAGAGCCGTTTATATGA 2416
 Db 2344 CTAAGAGAGGCAAGTGGGCTTTTGGGCTTAACATTAAGAGCTTCAATTAATGA 2403
 QY 2417 AATTAACTAGTCACTGAAACCAATGATGTAATCTTAATAAATTTAGAAATTCGA 2476
 Db 2404 AGTTAGCTTATGATG---AGATGATGTAATACTTGAA---CTTGGTTTCTGA 2456
 QY 2477 CTTAAGAAACATTAATTTACTGATGATGATGATGATGATGATGATGATGATGAT 2536
 Db 2457 CTTAATTAAC---TGTCAACCTGGCTCTCATGAACGTTGTTTCACTTCACTG 2513
 QY 2537 GAGTGCTCATTAAT 2552
 Db 2514 GAGTACTTCTGTGT 2529

RESULT 12
 ADU23192
 ID ADU23192 standard; cDNA, 2604 BP.
 XX
 AC ADU23192;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE Murine Toll-like receptor 6 (TLR6) cDNA sequence - SEQ ID 84.
 XX
 screening; Toll-like receptor agonist; TLR agonist; gene; ss; TLR6.
 XX
 OS Mus sp.
 XX
 PN W02004094671-A2.
 XX
 PD 04-NOV-2004.
 XX
 PR 22-APR-2004; 2004WO-US012788.
 XX
 PR 22-APR-2003; 2003US-0464586P.
 XX
 PR 22-APR-2003; 2003US-0464588P.
 XX
 PA (COLE-) COLEY PHARM GMBH.
 XX
 PA (COLE-) COLEY PHARM GROUP INC.
 XX
 PI Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
 DR WPLI, 2004-795573/78.
 XX
 PT Identifying agonists of Toll-like receptor (TLR) signaling activity.
 PT Useful therapeutically or prophylactically, comprises contacting an
 PT RPM18226 cell that expresses a TLR with a test compound and measuring TLR
 PT signaling activity.
 XX
 PS Disclosure; SEQ ID NO 84; 342pp; English.
 XX

CC The invention comprises a screening method for identifying agonists of
CC Toll-like receptor (TLR) signalling activity. The method involves
CC contacting an RPMI8226 cell (that expresses a TLR) with a test compound,
CC and measuring a test level of TLR signalling activity, where a test level
CC that is positive is indicative of a test compound that is a TLR agonist.
CC The method of the invention is useful for identifying agonists of TLR.
CC The present nucleic acid represents a TLR cDNA sequence.

XX Sequence 2604 BP; 689 A; 615 C; 561 G; 739 T; 0 U; 0 Other;

Query Match 55.7%; Score 1533.6; DB 13; Length 2604;

Best Local Similarity 76.1%; Pred. No. 0;

Matches 1930; Conservative 0; Mismatches 596; Indels 10; Gaps 3;

```
17 TCAAGATGCTCTGAAGAAGAACACCCCTTAGATAGCCATGCAACATCATGACCAAG 76
Db 4 TAAAAATGCTGGAAGAAATGTTAAAGTCCCTCTGGATAGCCTCTGCAACATGAGCCAA 63
Qy 77 ACAAGAACTATTTGTTAAAGCTTCATTTTGTGGCTTATGATCATATATGTTGAA 136
Db 64 ACAGAAACCCATCGTGGGAGTTTCCACTTTGTTGGCGCCTGGCCTTAATATGCGAA 123
Qy 137 CCAGATTCAGTTCTCCAGCGAATGAAATTGCACTAGACAAAGTCAAAAGAGCTTAA 196
Db 124 GCATGACCCCGTCTCTATGAACTTGAGTCTAGTACTATTTCAACAGAACTTAA 183
Qy 197 TTCATGTTCCAAAAGACCTACCGCTGAACCAAGTCTTAGATATGTTCTGAACTACA 256
Db 184 CTCATGTCCCAAAAGCTCGCCACCAAGAAACAAAGCCTGAGTCTGTCTCAAACTCTA 243
Qy 257 TCGCTGACCTTGAGGTCTCTGACATGAGCTTTCTATCAGAGTTGACAGTTTGAACCTT 316
Db 244 TATCTGAGCTTCGAGTGCCTGATATCAGCTTCTGTCAGAGCTGAGAGTTCTGACACTCT 303
Qy 317 CCCATTAAGATCCAGCTACTTGAATTGAAGTTTCAAGTTCAACCGAGATTGAAT 376
Db 304 CCCAAGACGATGAGGAGCCTTGATTTCCATGATTTCTGTTCAATCGAGACTTGAAT 363
Qy 377 ATTTGATTTATCTCATATCAGTTGCAAAAAGATATCTGCCATCTTATGAGATTCA 436
Db 364 ACCTGGAATGTCACACATGCTGTTGCAAAACATCTTGTGCTGCTTATGAGGAGCTGA 423
Qy 437 GGCATTTAGATCTCATTCATTCATGATTTCAAGCCCTGCGCATCTGTAAAGAAATTTGCA 496
Db 424 GGCATCTGAGCCTTCATTCATTCATGATTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 483
Qy 497 ACTTATCACAATGAAATTTCTGGATTTAGTGTCTGATGAAAGTGCAGAAATTTAGATTGCG 556
Db 484 ACCTGACGAAAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543
Qy 557 TGCCATTTGCTCACTTGATCTTAAGTTATCTTCTGATTTTAAAGAAATTTATATATA 616
Db 544 TCCCGATGCTCACTTGATCTTAAGTTATCTTCTGATTTTAAAGAAATTTATATATA 603
Qy 617 AAGAAATGAGACAGAAAGCTTACAAATTTCTGAATGCAAAAACCTTCACTTGTGTTTC 676
Db 604 AAGGGGGGAAACAGAAAGCTTTCAGATTTCCAAATTCACACCGTTCTCCATTGGCTTTC 663
Qy 677 ACCCAATGATTTATTCGATTCAGAGTGAACATATCAATTAATCTTAAGGTGCTTAC 736
Db 664 ATCCAAATAGCTTGTCTGTTCTGTTCAAGTGAACATGCTGTAAACGTTTAAAGACATTTTAC 723
Qy 737 AACTGACTATATTAATTAATGATGATGACAACTGTCAAGTTTTCATTAATTTTATACG 796
Db 724 AACTGAGTATATTAATTAATGATGATGACAACTGTCAAGTTTTCATTAATTTTATACG 783
Qy 797 AACTGACGAGGTTTCAACCTTATGAAATTTTAACTTCAACCAATAGAAACGACTTGA 856
Db 784 AACTGACGAGGTTTCAACCTTATGAAATTTTAACTTCAACCAATAGAAACGACTTGA 843
Qy 857 AATGCTGCTGAGAGCTTTTCAATTTCTTTGGCCCAACCTGTGGAATATCTCAATATTT 916
Db 844 AGTGTCTGCTTAACTTTTCAATTTCTTTGGCCCGACCGGTGAGTACTTCAATATTT 903
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Qy 917 ACAATTTAACAATATTAAGAACTTCGTGAAGAAATTTTACTTATTTCTAAACGACAT 976
Db 904 ACAATTTAACAATATTAAGAACTTCGTGAAGAAATTTTACTTATTTCTAAACGACAT 963
Qy 977 TGAAGCACTTGAACATTAATAATATATACGAAACCAAGTTTCTGTCTTCAAGACAGCTT 1036
Db 964 TGAAGCACTTGAACATTAATAATATATACGAAACCAAGTTTCTGTCTTCAAGACAGCTT 1023
Qy 1037 TGTACACCGGTGTTTCTGAGATGAACATTAATGATGATTAACCATTTACATCACCTTTTA 1096
Db 1024 TATACCTGCTGTTTCTGAGATGAACATTAATGATGATTAACCATTTACATCACCTTTTA 1083
Qy 1097 TACACATGCTGTGCTTCATGACCAACCAACCAATTAATTTTGAATTTTGAATTTTGAATTT 1156
Db 1084 TCCACATGCTGTGCTTCATGACCAACCAACCAATTAATTTTGAATTTTGAATTTTGAATTT 1143
Qy 1157 TTTTACAGATATATTTTGAAGAAATTTTCAAGTTTGAATTTTGAATTTTGAATTTTGAATTT 1216
Db 1144 TTTTACAGATATATTTTGAAGAAATTTTCAAGTTTGAATTTTGAATTTTGAATTTTGAATTT 1203
Qy 1217 TACAAAAAATGATTTAAAGAACTTTTCAAGTTTGAATTTTGAATTTTGAATTTTGAATTT 1276
Db 1204 TACAAAAAATGATTTAAAGAACTTTTCAAGTTTGAATTTTGAATTTTGAATTTTGAATTT 1263
Qy 1277 CTTTGAAGAAATGATTTAAAGAACTTTTCAAGTTTGAATTTTGAATTTTGAATTTTGAATTT 1336
Db 1264 CTTTGAAGAAATGATTTAAAGAACTTTTCAAGTTTGAATTTTGAATTTTGAATTTTGAATTT 1323
Qy 1337 GCATTTGGTGTGAAGATTAAGTGTGTTAAATTTTGTCTTCAAAATGCTTCTGACCTG 1396
Db 1324 GCGCTGGGCTGAAGAAATTTTGAAGAAATTTTGTCTTCAAAATGCTTCTGACCTG 1383
Qy 1397 TTTTCAAGATTTTCAAGTCAAGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1456
Db 1384 TCTTCAAGATTTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1443
Qy 1457 GCGTTCCTTAAACAATCGTAAACCTGAAAGCTTTTGAAGAACTCAATGTTTCTTCAAT 1516
Db 1444 GCATCCTTAAAGATGATCAACCACTGAGGCTTTTGAAGAACTCAATGTTTCTTCAAT 1503
Qy 1517 CTTTAACTGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1576
Db 1504 CTTTAACTGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1563
Qy 1577 ACAATTCAGTTTCCACCATCGGCTGATTTCTTCAAGTCTGACCTGACCAAGATGAGGTCAA 1636
Db 1564 ATTAATTCAGTTTCCACCATCGGCTGATTTCTTCAAGTCTGACCTGACCAAGATGAGGTCAA 1623
Qy 1637 TAAAGCAAGGAGCAATTCATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1696
Db 1624 TAAAGCAAGGAGCAATTCATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1683
Qy 1697 TAGACCAAGTATCAAGTGAAGTGAAGGCTGAGCTGATTTCTTAATGAAGTGAATGATGATG 1756
Db 1684 TAGGCTGGGTGCAAGAAAGTGAAGGCTGAGCTGATTTCTTAATGAAGTGAATGATGATGATG 1743
Qy 1757 CAGAAAGTTATAGAGAAAGCCCACTAAGGACTTTCATGATGATGATGATGATGATGATGATGAT 1816
Db 1744 CAGAAAGTTATAGAGAAAGCCCACTAAGGACTTTCATGATGATGATGATGATGATGATGATGAT 1803
Qy 1817 TAACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1876
Db 1804 CTGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1863
Qy 1877 CCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1936
Db 1864 TCCCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1923
Qy 1937 CTGCGGAGAGGCGAGAACTACCTTAGAAGAACTCAAGAAACCTCCAGTTTCAATG 1996
Db 1924 CCAGGCAAGGCGAGCAATCCCTTAGAAGAACTCAAGAAACCTCCAGTTTCAATG 1983
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QY 1997 CTTTATTTTCATATAGTGAACATGATTTCTGCTGGGTGAAAGTATTTGACTTACC 2056
 DB 1984 CTTTGTGTCTATACAGTGAAGCATGATTTCTGCTGGGTGAAAGATTTACTACCAACC 2043
 QY 2057 TAGAAAAAGATATACAGATTTTGTCTTCATAGAGAACTTTTCCCTGGCAGAGAGA 2116
 DB 2044 TAGAAGAAAGATATACATCCGGGTTTGGCTTCATAGAGAACTTTTCCCTGGCAGAGAGA 2103
 QY 2117 TTGTGAAAAATATCATCATCTGATTTGAGAGAGTACAAAGTCCATCTTTTGTGTCTC 2176
 DB 2104 TTGTGAGAACTCATCATCTTTCATTTGAGAGAGTTTACAGGCACTTTTGTGTCTC 2163
 QY 2177 CCAACTTTTGTCCAGAGTGAAGTGTGCTTACCAACTTATTTTGGCCATCAAACTCT 2236
 DB 2164 CCCACTTATTCAGAGTGAAGTGTGCTTACCAACTTATTTTGGCCATCAAACTCT 2223
 QY 2237 TTCTAGAAAGATCTATTAATCTTATCTTCTTACTTGAAGCCCATTCACAGAACAGA 2296
 DB 2224 TCCATGAAGGCTCTATTAATCTTATCTTCTTCTGTCGAAACCACTTCTACAGAACAGA 2283
 QY 2297 TTCCCAACAGTACCAAGCTGAAGGCTCTCATGACGAGGGACTTATTTGCAAGTGC 2356
 DB 2284 TTCCCAAGTATACCAAGCTGCGGCTCTCATGACGAGGGACTTATTTGCAAGTGC 2343
 QY 2357 CCAGAGAGAAAGCAACGCTGGCTCTTTGGGCTTACATTAAGCGGCTTTTAATATGA 2416
 DB 2344 CTACTGAGAGGGAACGCTGGCTTTTGGGCCAAGCTTGAAGCTTATTAATATGA 2403
 QY 2417 AATTACACTGATCTGCTGAAAACAATGATGTGAATCTTTAAAAAATTTAGAAAAATTCA 2476
 DB 2404 AGTTAGCTTGTGTCATG---AGGATGATGTGAATAAATTGAAA---CTTGGGTTTCTTA 2456
 QY 2477 CTTAGAGAAACATTTTACTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2536
 DB 2457 CTTATTAATAC---TGTCAACCTGGGCTCTCATGAACAGTGTGTTTCACTTCTAC 2513
 QY 2537 GAGTGCTCTCATTAAT 2552
 DB 2514 GAGTGCTCTCTGTGT 2529
 RESULT 13
 ADU23193
 ID ADU23193 standard; cDNA; 2421 BP.
 AC ADU23193;
 XX 27-JAN-2005 (first entry)
 DE Murine Toll-like receptor 6 (TLR6) cDNA sequence - SEQ ID 85.
 KM screening; Toll-like receptor agonist; TLR agonist; gene; ss; TLR6.
 OS Mus sp.
 PN MO2004094671-A2.
 XX 04-NOV-2004.
 PD 22-APR-2004; 2004WO-US012788.
 PF 22-APR-2003; 2003US-0464586P.
 PR 22-APR-2003; 2003US-0464586P.
 XX (COLE-) COLEY PHARM GMBH.
 PA (COLE-) COLEY PHARM GROUP INC.
 PI Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
 XX WPI; 2004-795573/78.
 PT Identifying agonists of Toll-like receptor (TLR) signaling activity,
 useful therapeutically or prophylactically, comprises contacting an

PT RPI8226 cell that expresses a TLR with a test compound and measuring TLR
 PT signaling activity.
 XX
 PS Disclosure; SEQ ID NO 85; 342bp; English.
 CC The invention comprises a screening method for identifying agonists of
 CC Toll-like receptor (TLR) signalling activity. The method involves
 CC contacting an RPI8226 cell (that expresses a TLR) with a test compound,
 CC and measuring a test level of TLR signalling activity, where a test level
 CC that is positive is indicative of TLR signalling activity, where a test level
 CC The method of the invention is useful for identifying agonists of TLR.
 CC The present nucleic acid represents a TLR cDNA sequence.
 SQ Sequence 2421 BP; 640 A; 586 C; 521 G; 674 T; 0 U; 0 Other;
 Query Match 55.6%; Score 1531.2; DB 13; Length 2421;
 Best Local Similarity 77.6%; Pred. No. 0;
 Matches 1848; Conservative 0; Mismatches 533; Indels 0; Gaps 0;
 63 CATCATGACCAAGCAAGAACCTATTTGTTAAAGCTTTCATTTTGTGCTTATGAT 122
 DB CAACATGAGCCAGACAGAAACCCATGCGGGAGTTTCCATTTGTTGCGCCCTGAC 89
 QY 123 CATATATGTTGGAAACCAAGATCCAGTTCTCCGACGGAATGAAATTTGCAAGACATC 182
 DB 90 CTTATATGTCGGAACATGACCCCGTTCTCTAATGAACTTATGATCTATGATGATATTC 149
 QY 183 AAAAGAGGCTTATTCATGTTCCAAAGAACCTACCGCTGAAACCAAGTCTTATGATAT 242
 DB 150 AAACAGGAACCTTATCTATGTCCTCCAAAGACCTGCCACCAAGAACAAAGCCCTGATCT 209
 QY 243 GTCTAGAACTACATCGCTGAGCTTCAAGTCTTCAAGTCTTCAATGATGATGATGATGATG 302
 DB 210 GTCTAAACCTTATATCTGAGCTTGGATGCTGATATGATGATGATGATGATGATGATGATG 269
 QY 303 AGTTTGAAGCTTTCCCAACAGATCCAGCTTATGATTTAAGTGTTCATGATTTCA 362
 DB 270 AGTTCTGAGCTCTCCCAACAGATCCAGCTTATGATTTAAGTGTTCATGATTTCTTCA 329
 QY 363 CCAGATTTAGAAATTTGATTTATCTCATTAATGATGATGATGATGATGATGATGATGATGATG 422
 DB 330 TCAGGACTTAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 389
 QY 423 TATTTGAGTTTCAAGGCTTATGATCTCTCATTTCAATTTCAAGGCTTCCCATCTG 482
 DB 390 TATGCGAGCTGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 449
 QY 483 TAAAGATTTGCAACTTATCAAACTGAATTTCTTGGATTTGAGTGTGATGATGATGATGATGATG 542
 DB 450 TAAAGATTTGCAACTTATCAAACTGAATTTCTTGGATTTGAGTGTGATGATGATGATGATGATG 509
 QY 543 AAAATTAATTTGCTGCAATTTGCTCACTTGCATTTAAGTTATTTCTTGGATTTAAG 602
 DB 510 ACAACTGATCTGCTCCAGTTGCTCACTTGCATTTAAGTTATTTCTTGGATTTAAGT 569
 QY 603 AAATTTATTTAATAAGAAATGAGACGAAAGTCTCAAAATTTCTGAATGCAAAAAACCT 662
 DB 570 GAGTTATCATTAATAAGGCGGGAACGAAAGTCTCAAAATTTCTGAATGCAAAAAACCT 629
 QY 663 TCACCTGTTTTCACCACTTATGATTTTCTGCTATCCAAAGTGAACATGATGATGATGATGATGATG 722
 DB 630 CCAATTTGCTTTCATTCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 689
 QY 723 TTTAGGCTGTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 782
 DB 690 TTTAGGATTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 749
 QY 783 TAAATTTTATCAAGATCAAGAGGTTCAACCTTCTGATTTTCCCAAGCCATCAT 842
 DB 750 GACATTTTATCAAGATCAAGAGGTTCAACCTTCTGATTTTCCCAAGCCATCAT 809
 QY 843 AGAAACGACTTGAAGGCTGTCAGAGTCTTCAATTTTGGCCCAAGCTGTGGA 902

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Db      810 AGAAACCAACCTGGAAGTCTGGTTAACTTTCCAAATCTTTTGACCCCGACCGGTGGA 869
Qy      903 ATATCTCAATATTATTAACAATTTAACAATATTGAAGACATTCGTGAAGAAATTTTACTTA 962
Db      870 GTACCTCAATATTATTAACAATTTAACAATATTGAAGAAATTCAGAGGAAGAAATTTACTTA 929
Qy      963 TTTTAAACGACATTGAAGACATTGACAAATGACAAATGACAAATGTTTCTGTT 1022
Db      930 CTCGAGACACGACGTAAGTCACTGATGATAGACACGTCAAACCAAGTGTCTCTCT 989
Qy      1023 TTCACAGACAGTTGTATACCCGTGTTTCTGAGATGAAACATTAATGATTTTCAATTTG 1082
Db      990 TTTCAAGGAGGCGCTATCTCGGTGTTGTAAGTAACATCAAGATGCTCTATCTTC 1049
Qy      1083 AGATACACCTTTTATACACATGCTGTGCTCATGACCAACGACATTCAAATTTTGA 1142
Db      1050 AGACACCCCTTTTATCCACATGATGTGCGCGCATCCCGACGCTATTTACATTTCTGA 1109
Qy      1143 CTTTACCAGAAACGTTTTACAGATAGTATTTTGAACAAATGTTCCAGCTTAAATTT 1202
Db      1110 CTTTACCAGAAATGTTTTTACTGACAGTGTGTTTCAAGGCTGTTCACCTTAAAGAAAT 1169
Qy      1203 GGAACACATTTATCTTACAAAAAATGATTTAAAGACCTTTTCAAAAGTGTCTATGAC 1262
Db      1170 GCAGACATTTATCTTACAAAGAAATGTTGAAGAACTTTTAAAGTGTCTATGAC 1229
Qy      1263 GAAGATATGCTCTTTTGAAGAAATGATGTTAGTGTGTTAAATTTGTCTTCAATAT 1322
Db      1230 TAAAGAAATGCTCTCTGGAACCTTTGAAATTTGTTGAATTTCTTGACCTTCATGAC 1289
Qy      1323 ACATTAAGAAAACTGCACTTGGGTTGAGAGTATGATGTTTAAATTTGTCTTCAATAT 1382
Db      1290 ATATGACAGGACATGCGCTGGGCTGAGAGCAATTTGGTGAATTTGTCTTCAATAT 1349
Qy      1383 GCTTATCACTCTGTTTTCAGATGTTTACTCTCCAGATGCAAGATGTTTCAACAG 1442
Db      1350 GCTTACAGGCTCTGTTCTCAGATGCTTACCTCCAGAGGCTTGAAGCTTGCACAA 1409
Qy      1443 CAATTAATTAAGAGCGTTCCATAACAGTCTTAACCTGAAGCTTGAAGAACTCA 1502
Db      1410 CAACAGGATTAATGACATCCCTTAAGATGTCAACCACTGACGGCTTTCAGAGAACTCA 1469
Qy      1503 TGTGCTTTCAATCTTTAACTGACCTTCTGATGTGGCAGCTTTAGACGCTTTCTGT 1562
Db      1470 TGTACATTCGAATCCTTAACTGACCTTCTGATGTGGGCTTTCAGAGCTTTCTGT 1529
Qy      1563 ATTGATCATGATTCACATTCAGTTTCCACCCATTCGCTGATTTTCTTCCAAAGCTGCA 1622
Db      1530 GCTGTCTATTCGACCAATTACTCAGTTTCCATCTCTGAGAAATTTCTTCCAGAGCTGCA 1589
Qy      1623 GAAGATGAGGTCAATTAAGAGCGGGAACATTCATTCATCTGATGAGCTTAAGAGA 1682
Db      1590 GAATATTGATTCCTTAACAGCGGGAACCAACCATTCATTCATGATGAGCTTAAGAGA 1649
Qy      1683 ATTTGTCAAAAATATAGACCAAGTATCAAGTGAAGTGAAGGCTGAGCTTATTTTA 1742
Db      1650 CTTTGTCAAGAACATAGGCTGGGTAGCAAGAAAGTGTGAGGCTGCTGACCTCTTA 1709
Qy      1743 TAACTGTGATCCAGAAAGTATTAAGAGAAACCCCACTAAAGGACTTTCATGATGTGA 1802
Db      1710 CAGGTGTGATCAACCAAGAAAGCTTAAGAGAACTGCACTGAGGAACTTCCACATGTCTCC 1769
Qy      1803 ATTATCTGCAACATTAATCTGCTGATGCTGACATCGGTGTCACATGCTGATGTGGC 1862
Db      1770 ACTGTCTGTGATTAATCTGCTGCTGATGCTGACATCGGAGGCACTATGCTGTGGC 1829
Qy      1863 TGTGATGTGACCTGCTCTGCTGCTGATCTATCTGATCTGCTGCTGATCTGATGCTG 1922
Db      1830 TGTGATGTGAGGCTTCTCTGCTGCTGCTGATCTGATCTGATGATGCTG 1889
Qy      1923 CCAGTGAACCCGATCTGGCGGAGGCGGAGAACTATCCCTTAAGAAAGCTCCAAAGAA 1982
Db      1890 TCAGTGAACACAGCACAGGCGGAGGCGGAGCAATCCCTTAAGAAAGCTCCAGAGAA 1949

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Qy      1983 CCTCAGTTTCATGCTTTTATTTATATATATAGTGAACATGATTTCTGCTGGGTGAAGTGA 2042
Db      1950 COTCAGTTTCATGCTTTTATTTGCTCATATACAGTACATGATATTTCTGCTGGGTGAAGTGA 2009
Qy      2043 ATTGATCTTAACTTACGAAAAAAGAAATATACATTTGTCTTATGAGAGAACTTTGT 2102
Db      2010 ATTACTTACCAACCTTACGAAAGATGATCATCCGGGTTTGGCTCCATGAGAGAACTTTGT 2069
Qy      2103 CCTGCAAGAGCATTTGGAAGAAATATCATCACTGATGAGAAAGTTTCAAGTCCAT 2162
Db      2070 CCTGCAAGAGCATTTGGAAGAAATATCATCACTGATGAGAAAGTTTCAAGTCCAT 2129
Qy      2163 CTTGTTTGTCTCCCACTTTGTCCAGAGTGAAGTGTGCTTATGAACTCTATTTTGC 2222
Db      2130 CTTTGTGCTGTCTCCCACTTATTCAGAGTGAAGTGTGCTTATGAACTCTATTTTGC 2189
Qy      2223 CCATACAAATCTCTTATCAATGAAAGATCTAATTAATCTCTCATCTTACGAAAGCCAT 2282
Db      2190 CCATCATATATCTCTTCAATGAAAGCTCTGATTAATCTCTCATCTTACGAAAGCCAT 2249
Qy      2283 TCCACAGAACAGCAATTCACCAAGTATACCAAGCTGAAGGCTCTCATGACGACGAGC 2342
Db      2250 TCTACAGAACACATTTCCAGTATACCAAGCTGCGGCTCTCATGACGACGAGC 2309
Qy      2343 TTATTTGCAGTGGCCCAAGAGAAAGCAACGTTGCTTTTGGGCTTAACTTTAGAC 2402
Db      2310 TTACTTGAATGCGCTACTGAGAAAGGCAACGTTGCTTTTGGGCTTAACTTTAGAC 2369
Qy      2403 CGCTTTTAAATTAATTAACATTAACATTAACATTAACATTAACATTAACATTAACAT 2443
Db      2370 TTTATTTATTTATGAAGTTAGCTTATGATCAATGAGAGATGATG 2410

RESULT 14
ADCT8820 standard; DNA; 2381 BP.
ID      ADCT8820
XX      ADCT8820;
XX      01-JAN-2004 (first entry)
XX      DE
XX      Human PRO protein coding sequence #25.
XX      KW
XX      human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
XX      Crohn's disease; gene; ds.
XX      OS
XX      Homo sapiens.
XX      PN
XX      WO2003034984-A2.
XX      PD
XX      01-MAY-2003.
XX      PF
XX      15-OCT-2002; 2002WO-US033070.
XX      PR
XX      19-OCT-2001; 2001US-0340083P.
XX      PA
XX      (GETH ) GENENTECH INC.
XX      FI
XX      Goddard A, Gurney AL;
XX      DR
XX      WPI, 2003-481990/45.
XX      P-PSDB; ADCT8821.
XX      PT
XX      New PRO polynucleotide and polypeptide, useful for the manufacture of a
XX      PT
XX      medicament for diagnosing or treating cancer or inflammatory bowel
XX      PT
XX      disorder e.g., ulcerative colitis or Crohn's disease.
XX      PS
XX      Claim 1; SEQ ID NO 49; 327bp; English.
XX      CC
XX      The invention comprises the amino acid and coding sequences of human PRO
XX      CC
XX      proteins. The DNA and protein sequences of the invention are useful for
XX      CC
XX      the diagnosis and treatment of cancer and inflammatory bowel disease

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CC (e.g. ulcerative colitis or Crohn's disease). The present DNA sequence
CC encodes a human PRO protein of the invention.
XX

Sequence 2381 BP; 725 A; 493 C; 450 G; 713 T; 0 U; 0 Other:

Query Match 52.5%; Score 1445; DB 10; Length 2381;
Best Local Similarity 76.3%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 550; Indels 6; Gaps 1;

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QY 84 ACCATATGTTAAAGCTTCATTTGTTGCTTATGATCATATATGTTGAACCGAAT 143
DB 11 ATCCAGACTAGCATCTTCATTTGCCATTTATCTTATGCTTAATCTCAGATCGAAT 70
QY 144 CCAGTCTCCGACGGAATGAAATTTGACAGACAGATCAAAAGAGCTTATTCATG 203
DB 71 ACAATATCTGAGAAAGTGAATTTTATGTTAGTCAAAACGAGTCAATCCACGT 130
QY 204 TCCAAAAGACCTACCGCTGAAAACAAAGCTTATGATATGTCAGAACTACATCGCTGA 263
DB 131 TCTTAAAGACTATCCGAGAAAACAACATCTTAAATATATGCCAAATTTATATCTGA 190
QY 264 GCTTCAGGCTCTGACATGACCTTTATACAGATTGACAGTTTGAGACTTCCATA 323
DB 191 GCTTGGACTTCGACATCTTATACCTGCAAAACGAGAGATTTGATTAATTTCTCAT 250
QY 324 CAGAAATCCAGTACTGATTTAAGTTTCAAGTTCAACGAGATTTGAATATTTGA 383
DB 251 TGAATTCAGTATCTTGATATACAGTCTTCAATTTCAACGAGAAATTTGAATATCTGA 310
QY 384 TTATATCTCAATACAGTTGCAAAAGATCTCCATCTTATGATGAGTTTCAAGCATTT 443
DB 311 TTGTGCCACAACAAGTTGATGAGATTTCTTGCCACCCATCGTAACTCAAGACATTT 370
QY 444 AATCTCTCATTCATGATTTTCAAGGCTCCGCCATCTGTAAGAAATTTGGCACTTATC 503
DB 371 GGACCTGTCATTTAAAGCATTTGATGCCCTGCTATATGCAAAAGATTTGGCAATATGTC 430
QY 504 ACAATGAAATTTCTGGATGATGAGTCTATGAAAGCGCAAAATTTGATTTGCTGCAT 563
DB 431 TCAATCAAAATTTCTGGGATGAGACCAACACTTGAAGAAATCTAGTGTGCTGCAT 490
QY 564 TCTCATCTGCATCTAAGTTATATCTTCTGATTTTGAAGAAATTTATATATAAGAAAA 623
DB 491 TGTCTATTTGAATATAGCAAGGCTTGTGCTGCTTATGAGAGACTTATGGGAAAAA 550
QY 624 TGAACAGAAAGCTTACAAATTTCTGATGCAAAACCTTCACTTTGTTTTCACCAAC 683
DB 551 AGACCTGAGGCTTCAAGACTTTTAACTGAGAGCTGACATTTGTTCCCCACAA 610
QY 684 TAGTTTATCGCTATCCAGTGAACATACAGTTAATCTTTAAGGCTGTTACACTGAC 743
DB 611 CAAAGAAATTCATTTATTTTATGATGTGACGCAAGACTGTAGCAAAATCTGAAATATC 670
QY 744 TAAATATTAAT-----TGAATGATGACAACTGTCAGATTTTCAATTAATTTTATCAGA 797
DB 671 TAAATCAAAATGTGTGCTAGAGATTAACAAATGTTCTTACTTCTTAAGTATTTCTGCCAA 730
QY 788 ACTCACAGAGGTTCACTTACGAAATTTTACCTTCAACCAATAGAAAGACCTTTGAA 857
DB 721 ACTTCAAACTAAATTCAAAGTTATCAAGTCTTACCTTAAACAATTTGAACAATCTTGAA 790
QY 858 ATGCTGCTCAGAGCTTTTCAATTTCTTGCCCAAACTGTGGAATATCTCAATTTTA 917
DB 791 TTTCTTCAATAGAGTCTCTCAGCTGATTTGCAATACCTGATGATTTTCTCAATTTTC 850
QY 918 CAATTTAACTAATTTGAAAGCATTCGTGAGAGAAATTTTACTTATTTTAAACGACAT 977
DB 851 AAACGTGAAGCTACAGGGCTCAGCTGACCTTCAAGATTTTGAATATTTCTGGACATTCCT 910
QY 978 GAAACATTTGACAAATAGACATATACGAAACAAGTTTCTGTTTTCACAGACATTT 1037
DB 911 GAAAGCTTGTGTATACCAACAAAGTGTGTGAGCATGTGTGCTTCCGCAAAATTTATAT 970
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QY 1038 GTACACCGTGTGTTTCTGAGATGAACATTAATGTTAACTTTCAGATACACTTTTAT 1097
DB 971 CTATGAAATCTTTTGCATATGACATCAAAATTTTCAAGTCTGTGATACGACATGCT 1030
QY 1098 ACACATGCTGTGTCTCATGACCAAGCAATTCAGATTTTGAACCTTACCAGAACGT 1157
DB 1031 CCACATGCTTTGGCCATCCAAATATATGACCGTCTCGCATTTGGATTTTCCAAATATCT 1090
QY 1158 TTTTCAAGATAGTATTTTGAAGAAATGTTCCACGTTAAGTTAATTTGAGACATTTCTT 1217
DB 1091 CTTAAACAGACAGGTTTGAAGAAATTTGGGACCTTACTGATGTTGGAACCTTATTTT 1150
QY 1218 ACAAAAAATGATTTTAAAGACCTTTTCAAGAGGCTTCATGACAGAGATATGCTTCC 1277
DB 1151 ACAATGAAATCAATTTAAAGAACTTTCAAAATATGCTGAATGACTACACAGTGAAGTC 1210
QY 1278 TTTGGAATATCTGATGATTTAGCTGGAATTTCTTGAATCTGTGATGACATTAAGAAAAC 1337
DB 1211 TCTGCAACAAATTTGAAATATGACAGAAATTTCTGTAAGCTATGATGAAGAAAGAGAC 1270
QY 1338 CACTGGGTTGAGAGATATGCTGTAAATTTGCTTCAATATGCTTACTGACTCTGT 1397
DB 1271 TTTCTGCACTAAAGATTTTAAAGTTTAAATATGCTTCAAAATATCTTACTGACACTAT 1330
QY 1398 TTTTCAAGATTTTACCTCCAGGATCAAGGATCAAGTACTTATCTTCAAGCAATTAATAAGAG 1457
DB 1331 TTTTCAAGATTTTACCTCCAGGATCAAGGATCAAGTACTTATCTTCAAGCAATTAATAAGAG 1390
QY 1458 CGTTCTTAAACAAGTCTTAAACCTGGAACCTTTGCAAGAACTCAATGTTGCTTCAATTC 1517
DB 1391 CATCTCTTAAACAAGTCTTAAACCTGGAACCTTTGCAAGAACTCAATGTTGCTTCAATTC 1450
QY 1518 TTTTAACTGACCTTCTGATATGCTGAGACCTTTTACAGACCTTTCTGATTTATCATTTGATCA 1577
DB 1451 TTTTAACTGACCTTCTGATATGCTGAGACCTTTTACAGACCTTTCTGATTTATCATTTGATCA 1510
QY 1578 CAATTCAGTTTCCACCCCATGCGCTGATTTCTTCCAGAGCTCCAGAAATAGAGCTCAT 1637
DB 1511 CAATTCAGTTTCCACCCCATGCGCTGATTTCTTCCAGAGCTCCAGAAATAGAGCTCAT 1570
QY 1638 AAAACGAGGGGCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1697
DB 1571 AAAACGAGGGGCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1630
QY 1698 AGACCAAGTATCAAGTGAAGTGTGAGAGGCTGCTGATTTCTTAAAGTGTGATCACTCC 1757
DB 1631 AGACCAAGTATCAAGTGAAGTGTGAGAGGCTGCTGATTTCTTAAAGTGTGATCACTCC 1690
QY 1758 AGAAGTTATAGAGAAAGCCCTAAGGACCTTCAACATGCTGAATTAATCTGCAACAT 1817
DB 1691 GGAAGTTATAGAGAAAGCCCTAAGGACCTTCAACATGCTGAATTAATCTGCAACAT 1750
QY 1818 AACTGTGATGATGATCACCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1877
DB 1751 AACTGTGATGATGATCACCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1810
QY 1878 CCTGTGATCTTACTTGGATCTGCTGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 1937
DB 1811 CCTGTGATCTTACTTGGATCTGCTGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 1870
QY 1938 TCGGGGAGGGGCAAGAACTACCTTGAAGAACTCCAAAGAAACCTCCAGATTTATGCTC 1997
DB 1871 CCGGGGAGGGGCAAGAACTACCTTGAAGAACTCCAAAGAAACCTCCAGATTTATGCTC 1930
QY 1998 TTTTATTTCAATATGATGAACATGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 2057
DB 1931 ATTATTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1990
QY 2058 AGAAAAAGAAATATACAGATTTGCTTCAAGAGAACTTTGCTGCTGATGATGATGATGATGATGAT 2117
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Qy 2358 CAAGGAAAGAAAGCAAGCTGAGCTCTTTTGGGCTAACTTAAGGCGCTTTAATATGA 2417
Db 2291 CAAGGAAAGAAAGCAAGCTGAGCTCTTTTGGGCTAACTTAAGGCGAGCCATTAATATGA 2350
Qy 2418 ATTAAACA 2424
Db 2351 GCTGACA 2357
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RESULT 15

ADE25536
ID ADE25536 standard; DNA; 2358 BP.

AC ADE25536;

XX 29-JAN-2004 (first entry)

XX Human TLRI related DNA SEQ ID NO 2.

XX Human; TLRI; cancer; cyrostatic; ds; gene.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..2358

FT FT /tag= a

FT FT /product= "TLRI"

FT FT /partial

XX /note= "the CDS lacks a stop codon"

XX MO2003061697-A1.

XX 31-JUN-2003.

XX 26-DEC-2002; 2002WO-JP013642.

XX 27-DEC-2001; 2001JP-00398165.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Hikichi Y, Katsuyama R, Kakoi Y, Nishizawa S;

XX WPI: 2003-598709/56.

XX P-PSDB; ADE25535.

XX Treatment and prevention for cancer of the e.g. digestive system, liver

XX and lung.

XX Disclosure; Page 80-84; 98pp; Japanese.

XX The invention relates to the treatment and prevention of cancer

XX comprising a compound that inhibits the activity of protein or peptide

XX fragment of a fully defined amino acid sequence TLRI given as SEQ ID NO

XX 1. TLRI is useful in the treatment and prevention of cancers of the large

XX intestine, mammary glands, lung, prostate, digestive tract, stomach and

XX liver. TLRI gene expression is detected in breast cancer tissue. The

XX present sequence is that of a human TLRI encoding DNA sequence.

Seq Sequence 2358 BP; 720 A; 486 C; 444 G; 708 T; 0 U; 0 Other;

Query Match 52.5%; Score 1444.2; DB 10; Length 2358;

Best Local Similarity 76.4%; Pred. No. 0;

Matches 1789; Conservative 0; Mismatches 548; Indels 6; Gaps 1;

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GenCore version 5.1.9
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(without alignments)
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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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ALIGNMENTS

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DEFINITION Sequence 79 from Patent WO2004094671.
ACCESSION CQ903893
VERSION CQ903893.1 GI:55785292
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 Vollmer, J., Jurk, M., Lipford, G.B., Schetter, C., Forsbach, A. and
Krieg, A.M.

TITLE Methods and products for identification and assessment of tlr
ligands

JOURNAL Patent, WO 2004094671-A 79 04-NOV-2004;
Coley Pharmaceutical GmbH (DE); Coley Pharmaceutical Group, Inc.
(US)

FEATURES
source location/Qualifiers
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/mol_type="unassigned DNA"
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ORIGIN

Query Match 100.0%; Score 2753; DB 2; Length 2753;
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Matches 2753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	2461	AATTTAGAAATTCACCTTAAGAAACCATTTATTTACTTGATGATGTGAATAGTACAGT	2520
QY	2521	CGTAGTAACTGCTCGAGAGTGCCCTCCATTATCTCATTGCTTCAAGAAAACTTAACAA	2580
Db	2521	CGTAGTAACTGCTCGAGAGTGCCCTCCATTATCTCATTGCTTCAAGAAAACTTAACAA	2580
QY	2581	AAACAATGTTTCATCTGGAGAACTAGTAAAGCGGTAGGTTAGCTGCCAGTTAGAGAC	2640
Db	2581	AAACAATGTTTCATCTGGAGAACTAGTAAAGCGGTAGGTTAGCTGCCAGTTAGAGAC	2640
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Db	2641	AGCCAGTCTCTTGTTTAATCATATATGTTTCAAAATGGAACAGTCTCTTTTGAATAA	2700
QY	2701	ATGCTCAATTTTTCAGCTCTCTCCACTCTGCTTTCCAAATGGAATTCGTG	2753
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RESULT 2			
CQ726557			
LOCUS	CQ726557	2758 bp	DNA
DEFINITION	Sequence 12491 from Patent WO02068579.	linear	PAT 03-FEB-2004

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE	AUTHORS	TITLE
1	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.	Kites, such as nucleic acid arrays, comprising a majority of humaneons or transcripts, for detecting expression and other uses

thereof
Patent: WO 02068579-A 12491 06-SEP-2002;
PE Corporation (NY) (US)

FEATURES	Location/Qualifiers
source	1. .2758

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/organism="Homo sapiens"  
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	ORIGIN
Query Match	99.9%; Score 2749.8; DB 2; Length 2758;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 2751; Conservative	0; Mismatches 2; Indels 0; Gaps 0.

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Db 2 AGAATTTGGACTCATATCAAGATGCTCTGAGAAGAACCAACCTTTAGATAGCCACTGC 61

QY 61 AACATCATGACCAAGAACAAGAACCTATTGTTAAAGCTTCATTTGTTGGCCATTAG 120

Db 62 AACATCATGACCAAGAACAAGAACCTATTGTTAAAGCTTCATTTGTTGGCCATTAG 121

QY 121 ATCATATATGTTGGAAACCAAGATCCAGTCTCCGACGGAATATATTTGCAGTAGACAAG 180

Db 122 ATCATATATGTTGGAAACCAAGATCCAGTCTCCGACGGAATATATTTGCAGTAGACAAG 181

QY 181 TCMAAAGAAGGCTTATTTTCATGTTCCMAAAGACTTCCGCTGAAAACCAAAAGCTTTAGAT 240

Db	182	TCAAAAAGAGGCTCTTATTCATGTTCCAAAAGAACTCAACCGCTGGAAAAACCAAGTCTTAGAT	241
OY	241	ATGCTCAGAACTACATCGCTGAGCTTCAGGCTCTGACATGAGCTTTCTATCAGAGTTG	300
Db	242	ATGCTCAGAACTACATCGCTGAGCTTCAGGCTCTGACATGAGCTTTCTATCAGAGTTG	301
OY	301	ACAGTTTGGAGCTTTCCATPACAGAAATCCAGCTACTTGAATTTAAGTGTTCAGAGTTC	360
Db	302	ACAGTTTGGAGCTTTCCATPACAGAAATCCAGCTACTTGAATTTAAGTGTTCAGAGTTC	361
OY	361	AACGAGGTTTAGAATATTGGATTTATTCATATACATGTCGAAAGATATCCGTGCAT	420
Db	362	AACGAGGTTTAGAATATTGGATTTATTCATATACATGTCGAAAGATATCCGTGCAT	421
OY	421	CCATATTGGAGTTTCAGGCACTTTCAGATCTCATTTCAATGATTTCAAGGCCCTGCCATC	480
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OY	481	TGTAAGGAATTTGGCAACTATACAACTGAATTTCTTGGATTAAGTGTATGAAGCTG	540
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Db	962	TATTTCTAAAAAGCACTTGAAGACATTGACATAGAACATATCAGAAACCAAGTTTTCTG	1021
OY	1021	TTTTTCAAGACAGTTTGTATACACCGTGTTTTCTGAGATGGAACATTTAAGTTTAAACATT	1080
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Db	1082	TCAGATACACCTTATATACACATGCTGTGTCCTATGACACCAAGACATTCAGTTTTTG	1141
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QY	1561	GTATTGATCA	TGATGATCAATTCAGTTTCC	AGCCCATGAGTGAATTTCTTC	1620		
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QY	1621	CAGAAAGATGAGTCA	TATAAGCGGGGACA	TCCATTCGAAATGATCCTG	TGAGACTTAA	1680	
Db	1622	CAGAAAGATGAGTCA	TATAAGCGGGGACA	TCCATTCGAAATGATCCTG	TGAGACTTAA	1681	
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QY	1861	GCTGTGACTG	ACCTCCCTCTGCACT	CTACTGATCTGCCCTGAT	CTTCAGATGGT	1920	
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QY	2101	GTCCCTGGCA	AGAGATGTTGAAAAAT	TTCATCACTGAAAGATTA	CAAGTCC	2160	
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Db	2162	ATCTTTGTTTGT	CTCCCACTTTGT	CCAGAGTGA	GTGGCCATTA	CGAATCTATATTT	2221
QY	2221	GCCCATCA	TCATCTTTCATGAAGAT	CTAATAATTCCTAT	CTTA	CTGAAACC	2280
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QY	2701	ATGCTCAGTTTTGAGCTCTCTTCOACTCTGCTTTCCCAATGGATTTCTGTG	2753
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RESULT 3			
AR659471			
LOCUS	2758 bp	DNA	linear
DEFINITION	Sequence 226 from patent US 6900016.		PAT 13-JUN-2005

VERSION AR659471.1 GI:67595477

SOURCE Unknown.

Unclassified

REFERENCE	DATE
Yenter, J. C., Zhang, J.	2021

TITLE Polymorphisms in known genes associated with inflammatory

Patent: US 6,900,016-A 226 31-MAY-2005:

FEATURES
Applera corporation; Norwalk, CT
Location/Qualifiers

source
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Best Local Similarity 99.9%; Pred. No. 0;

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RESULT 4

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LOCUS Sequence 672 from patent US 6900016.
ACCESSION AR659631
VERSION AR659631.1 GI:67595671
KEYWORDS
SOURCE
ORGANISM

REFERENCE

1 (bases 1 to 6758)
Unclassified.
Venter, J.C., Zhang, J.N., Liu, X., Rowe, W., Cravchik, A., Kalush, F.,
Nak, A., Subramanian, G. and Woodage, T.
Polymorphisms in known genes associated with inflammatory
autoimmune disease, methods of detection and uses thereof
Patent: US 6900016-A 672.31-MAY-2005;
Apliera Corporation; Norwalk, CT

JOURNAL

FEATURES
source

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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 99.9%; Score 2749.8; DB 2; Length 6758;
Best Local Similarity 99.9%; Pred. No. 0;
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QY 61 AACATCATGACCAAGACAAAGAACCTATTGTTAAAGCTTCATTGTTGCTTATG 120
DB 2062 AACATCATGACCAAGACAAAGAACCTATTGTTAAAGCTTCATTGTTGCTTATG 2121
QY 121 ATCATATATGTTGGAACCAAGATCCAGTTCTCCAGAGAAATGAATTTGAGTAGACAG 180
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QY 181 TCAAAAAGAGGCTTATTCATGTTCCAAAAGACCTACGCTGAAAACCAAAGTCTAGAT 240
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DB 2302 ACAGTTTGAAGCTTTCCATAACAGAAATCCAGCTACCTGATTTAAAGTGTTCAGATTTC 2361
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QY 1501 AATGTTGCTTCAATTTCTTTAACTGACCTTCTGAGATGTGGAGCTTTTACGACCTTTCT 1560

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O	y	1561	GTATTGATCATTTGATCACAAATTCAGTTTCCACCCATCGGCTGATTTCTTCCAGAGCTGC	1620
D	b	3562	GTATTGATCATTTGATCACAAATTCAGTTTCCACCCATCGGCTGATTTCTTCCAGAGCTGC	3621
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O	y	1681	GAATTTGTCAAAAAATATAGACCAGATTCACAGTGAAGTTTAGAGGGCTGGCTCAATCT	1740
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Db 4702 ATGCTCAGTTTTCAGCTCCTCTCCAGCTGCTTCCCAAGGATTCGTGG 4754

RESULT 6
AC108044/c 173834 bp DNA linear PRI 29-MAY-2002
LOCUS Homo sapiens BAC clone RP11-280E3 from 4, complete sequence.
DEFINITION AC108044
ACCESSION AC108044.5 GI:20304050
VERSION HTG.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 173834)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
9847074
PUBMED

REFERENCE
AUTHORS Nguyen,C., Abdolt,A., Bielicki,L. and Spalding,L.
TITLE The sequence of Homo sapiens BAC clone RP11-280E3
JOURNAL Unpublished (2001)
REFERENCE
AUTHORS 3 (bases 1 to 173834)
TITLE Waterston,R.H.
JOURNAL Direct Submission
Submitted (24-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 173834)
Waterston,R.H.
Direct Submission
Submitted (25-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 173834)
Waterston,R.H.
Direct Submission
Submitted (25-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 173834)
Waterston,R.
Direct Submission
Submitted (29-MAY-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Apr 25, 2002 this sequence version replaced gi:20128729.

REFERENCE
AUTHORS Center: Washington University Genome Sequencing Center
TITLE Center code: WUGSC
JOURNAL Web site: <http://genome.wustl.edu/gsc>
COMMENT Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH028003

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.

McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Moon,P.Y., Zhao,B., Frengen,E., Tareno,M., Catanes,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-427122, the clone sequenced to the right is RP11-360F5. Actual start of this clone is at base position 1 of RP11-280E3; actual end is at base position 173834 of RP11-280E3.

FEATURES

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 49519 ATGCTCAGAACTACATCGCTGAGCTTCAAGCTCTGACATGATGAGCTTTCTATCAGAGTTG 49460
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VERSION      CO870747.1      GI:52000200
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REFERENCE
AUTHORS      Hardiman,G.T., Rock,F.L., Bazan,J.F., Kastelein,R.A., Ho,S.W. and
              Liu,Y.J.
TITLE      Human receptor proteins, related reagents and methods
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ORIGIN

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LOCUS CQ903892
DEFINITION Sequence 78 from Patent WO2004094671.
ACCESSION CQ903892
VERSION CQ903892.1 GI:55785291
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

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REFERENCE
AUTHORS Vollmer, J., Jurk, M., Lipford, G.B., Schetter, C., Forsbach, A. and
Krieg, A.M.
TITLE Methods and products for identification and assessment of rlr
ligands
JOURNAL Patent: WO 2004094671-A 78 04-NOV-2004;
Coley Pharmaceutical GmbH (DE); Coley Pharmaceutical Group, Inc.
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FEATURES
SOURCE location/Qualifiers
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Query Match 99.8%; Score 2748.8; DB 2; Length 2760;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2750; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 902 GAATATCTCAATATTTTCAATTTTAACTAATTTGAAGCAATTCGTGAAGAAATTTTACT 961

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ACCESSION	AR659345		
VERSION	AR659345.1	GI:67595337	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2760)		
AUTHORS	Venter, J. C., Zhang, J. N., Liu, X., Rowe, W., Cravchik, A., Kalush, F., Maik, A., Subramanian, G. and Woodedge, T.		
TITLE	Polymorphisms in known genes associated with inflammatory autoimmune disease, methods of detection and uses thereof		
JOURNAL	Patent: US 6900016-A 100 31-MAY-2005; Aplera Corporation; Norwalk, CT		
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DEFINITION Sequence 40 from Patent WO0190151.
ACCESSION AX399047
VERSION AX399047.1 GI:21261430
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AUTHORS
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 Homnidae; Homo.
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 Takeuchi,O., Kawai,T., Sanjo,H., Copeland,N.G., Gilbert,D.J.,
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 TLR6: A novel member of an expanding toll-like receptor family

JOURNAL Gene 231 (1-2), 59-65 (1999)
PUBMED 10231569
REFERENCE 2 (bases 1 to 2760)
AUTHORS Akira, S. and Takeuchi, O.
TITLE Direct Submission
JOURNAL Submitted (05-DEC-1998) Shizuo Akira, Hyogo College of Medicine,
Department of Biochemistry, Mukogawa-cho 1-1, Nishinomiya, Hyogo
663-8501, Japan (E-mail:sakira@biken.osaka-u.ac.jp,
Tel:81-798-45-6357, Fax:81-798-46-3164)

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 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo
 1 (bases 1 to 78986)
 Waterston, R.H.
 The sequence of Homo sapiens clone
 Unpublished
 2 (bases 1 to 78986)
 Waterston, R.H.
 Direct Submission
 Submitted (21-MAR-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Mar 21, 2002 this sequence version replaced gi:8076856.
 COMMENT
 ----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 Contact: submissions@watson.wustl.edu
 ----- Project Information -----
 Center project name: H_NH0685M06
 Drafting center: WIBR
 ----- Summary Statistics -----
 Sequencing vector: M13, 0%
 Sequencing vector: plasmid, 100%
 Chemistry: Dye-terminator Big Dye, 100% of reads
 Chemistry: Dye-terminator Big Dye, 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 64210 bases at least Q40
 Consensus quality: 67703 bases at least Q30
 Consensus quality: 69979 bases at least Q20
 Insert size: 17700; agarose-fp
 Insert size: 73365; sum-of-ctnigs
 Quality coverage: 0.81 in Q20 bases; agarose-fp
 Quality coverage: 2.05 in Q20 bases; sum-of-ctnigs
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 43 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 * 1133 2884: contig of 1752 bp in length
 * 2885 2984: gap of unknown length
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 * 6551 8317: gap of unknown length
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13971	15716:	contig of 1746 bp in length
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15817	18126:	contig of 2310 bp in length
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18227	19694:	contig of 1468 bp in length
19695	19794:	gap of unknown length
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33288	34703:	contig of 2316 bp in length
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Best Local Similarity	99.9%;	Pred. No. 0;	
Matches 2750;	Conservative 0;	Mismatches 3;	Indels 0; Gaps 0;

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 DB 46744 AGAATTGGACCTATATCAAGATGCCTCTGAAGAAGAACAAACCCCTTTAGATGCGACTGCC 46685

QY 61 AACATCATGACCAAGACAAAGAACCTATGTTAAAAAGCTTCATTTGTTGCTTATG 120
Db 46684 AACATCATGACCAAGACAAAGAACCTATGTTAAAAAGCTTCATTTGTTGCTTATG 46625
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QY 241 ATGCTCAGAACTACATCGCTGAGCTTCAGGCTCTGACATGAGCTTTCTATCAGAGTGG 300
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Db 46444 AAGATTTTGAAGCTTTCCATAACAGAAATCCAGTACTGATTAAGTGTTCAAAGTTC 46385
QY 361 AACCAAGATTTGAATATTTGATTTATCTCAATTAATCAGTTGAAAAGATCCGCTGAT 420
Db 46384 AACCAAGATTTGAATATTTGATTTATCTCAATTAATCAGTTGAAAAGATCCGCTGAT 46325
QY 421 CCTATGTTGAGTTTGAAGCAATTTAGATCTCTCATTCATGATTTTCAAGGCTCCGCTATC 480
Db 46324 CCTATGTTGAGTTTGAAGCAATTTAGATCTCTCATTCATGATTTTCAAGGCTCCGCTATC 46265
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Db 46204 CAAAAATTAAGATTTGCTGCAATTTGCTCATCTGCAATTAATTTCTTCTGAGTTTA 46145
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ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 182019)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 4, clone RP11-11518
Unpublished
2 (bases 1 to 182019)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavsky,L.,
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TITLE
JOURNAL
REFERENCE
AUTHORS

Zody,M.
Direct Submission
Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 182019)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
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Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 12, 2000 this sequence version replaced gi:7229904.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MWR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information -----
Center project name: 115.L.8
Center clone name: 115.L.8

----- Summary Statistics -----
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Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
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Insert size: 179319; sum-of-ctnigs
Quality coverage: 5.2 in Q20 bases; agarose-fp
Quality coverage: 3.8 in Q20 bases; sum-of-ctnigs

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NOTE: This is a 'working draft' sequence. It currently
* consists of 28 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1332: gap of 100 bp
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	*	43880	43879: contig of 3919 bp in length
	*	43880	43879: gap of 100 bp
	*	43980	48725: contig of 4746 bp in length
	*	48726	48825: gap of 100 bp
	*	48826	53473: contig of 4648 bp in length
	*	53474	53573: gap of 100 bp
	*	53574	59514: contig of 6641 bp in length
	*	59515	59714: gap of 100 bp
	*	59715	65908: contig of 6194 bp in length
	*	65909	66008: gap of 100 bp
	*	66009	72470: contig of 6662 bp in length
	*	72471	72570: gap of 100 bp
	*	72571	79694: contig of 7124 bp in length
	*	79695	79794: gap of 100 bp
	*	79795	87082: contig of 7288 bp in length
	*	87083	87182: gap of 100 bp
	*	87183	99295: contig of 1213 bp in length
	*	99296	99395: gap of 100 bp
	*	99396	114225: contig of 14830 bp in length
	*	114226	114325: gap of 100 bp
	*	114326	128932: contig of 14607 bp in length
	*	128933	129032: gap of 100 bp
	*	129033	143986: contig of 14954 bp in length
	*	143987	144086: gap of 100 bp
	*	144087	160372: contig of 16286 bp in length
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DEFINITION Novel Toll-like receptor and gene thereof.
ACCESSION E34464
VERSION E34464.1 GI:18624350
KEYWORDS JP 2000128900-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 2760)
 AUTHORS Shindra,S. and Takeuchi,S.
 TITLE Novel Toll-like receptor and gene thereof
 JOURNAL Patent: JP 2000128900-A 1 09-MAY-2000;
 SCIENCE & TECH AGENCY

COMMENT

OS Homo sapiens (human)
 PN JP 2000128900 -A/1
 PD 09-MAY-2000
 PF 26-OCT-1998 JP 1998304110

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GenCore version 5.1.9
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1439.4	52.3	2806	6	HSN800268 Mus muscu
7	1267.4	46.0	3051	10	DY109015 Homo sapi
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24	464.4	16.9	829	9	DN935328	DN935328
25	462.6	16.8	630	12	CL003155	CL003155
26	462.4	16.8	568	9	DB140065	DB140065
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25	462.6	16.8	630	12	CL003155	CL003155
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29	429.2	15.6	485	7	BE006232	BE006232
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ALIGNMENTS

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PUBMED
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AUTHORS
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JOURNAL
COMMENT
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source
gene
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GSS.
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Hominidae; Homo.
1 (bases 1 to 2391)
Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 2391)
Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submision
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2389; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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REFERENCE 1 (bases 1 to 2391)
 Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civiello, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)

JOURNAL PUBLISHED 14671302
 2 (bases 1 to 2391)
 Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civiello, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.

TITLE Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment

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 Db 1081 ACCCGAAACGTTTTCACAGATATGATTTTGAAGATTTTCACGTTAGTTAAATGAG 1140
 QY 1207 ACACCTTATCTTAACAAAAAATGATTAAGACCTTTCAAGTATGATGCTATGACGAAG 1266
 Db 1141 ACACCTTATCTTAACAAAAAATGATTAAGACCTTTCAAGTATGATGCTATGACGAAG 1200
 QY 1267 GATATGCTCTTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1326

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Db      1261 AAGAAAACTGCACTGGGTGAGAGTATAGTGTGTTAAATTTGGCTCAATATGTCT 1320
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Db      1621 GTCAAAAATATATGACCAAGTATCAAGTGAAGTGTAGAGAGGCTGGCTGATTTCTTATTAAG 1680
Qy      1747 TGTGACTACCCAGAAAGTTATAGAGAAAGCCCACTAAAGACTTTTCACTGTCTGAATTA 1806
Db      1681 TGTGACTACCCAGAAAGTTATAGAGAAAGCCCACTAAAGACTTTTCACTGTGAATTA 1740
Qy      1807 TCCTGCAACATTAATCTCTGTATTCGTACCAATCGGTGCCACATGCTGTGTGGCTGTG 1866
Db      1741 TCCTGCAACATTAATCTCTGTATTCGTACCAATCGGTGCCACATGCTGTGTGGCTGTG 1800
Qy      1867 ACTGTGACCTCTCTGTGATCTACTGTGATCTGCCCTGTGATCTCAGATGTGTGCCAG 1926
Db      1801 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1860
Qy      1927 TGGACCCAGACTCGGCGAGGCGAGCAATACCTTTAGAAAGCTCCCAAGAAACCTC 1986
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Qy      1987 CAGTTTCATGCTTTTATTTCAATATAGTGAACATGATTTCTGCTGGGTGAAAAGTGAATTG 2046
Db      1921 CAGTTTCATGCTTTTATTTCAATATAGTGAACATGATTTCTGCTGGGTGAAAAGTGAATTG 1980
Qy      2047 GTACCTTCTCTGAAAAAGAAATATATACGATTTGTCTTCATGAGAGAACTTTGCCCCCT 2106
Db      1981 GTACCTTCTCTGAAAAAGAAATATATACGATTTGTCTTCATGAGAGAACTTTGCCCCCT 2040
Qy      2107 GGCAGAGAGATTTGGAAAAATATATCACTCACTGAGAAAGATTACCAAGTCAATCTTT 2166
Db      2041 GGCAGAGAGATTTGTGAAAAATATATCACTCACTGAGAAAGATTACCAAGTCAATCTTT 2100
Qy      2167 GTTTTGTCTCCCACTTTTGTCCAAGTGAAGTGTGCTGATTCAGAACTGATTTTGGCCAT 2226
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Qy      2227 CACATTCCTTTCAAGAAAGATCTAATACTTAATCTTCACTTCACTTGAAGCCCATTTCA 2286
Db      2161 CACATTCCTTTCAAGAAAGATCTAATACTTCACTTCACTTGAAGCCCATTTCA 2220
Qy      2287 CAGAACAGATTTCCCAACAAGTACCAACAAGTGAAGGCTCTCATGACGAGCGGACTTAT 2346
Db      2221 CAGAACAGATTTCCCAACAAGTACCAACAAGTGAAGGCTCTCATGATGACGCGGACTTAT 2280
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RESULT 3
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sequence.
ACCESSION
AKI37502
VERSION
AKI37502.1 GI:74210384
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
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Kono, H., Akiyama, U., Nishi, K., Kitesuna, T., Tashiro, H., Itoh, M.,
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Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kiry, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multiplexed sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, O., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamahata, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
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Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, T., Pezole, G.,
Quackenbush, D., Schriml, L.M., Stubli, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
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Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gestrich, S., Hill, D.,
Hofmann, M., Hume, D.A., Kamita, M., Lee, N.H., Lyons, P.,
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and Hayashizaki, Y.
RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

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Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Ball, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batilov, S., Beisel, K.W., Blake, J.A., Brad, D., Bruscia, V., Chochia, C., Cordani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Fraser, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglot, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Perlea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sadelain, A., Schneider, C., Sempke, C.A., Setou, M., Shimada, K., Sulana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, K., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

PANTOM Consortium

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420 (6915), 563-573 (2002)

12466851

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Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Bremner, S.E., Batilov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Altans, V., Allen, J.E., Ambesi-Impombato, A., Apweiler, R., Atturliya, R.N., Bailey, T.L., Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., Di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furum, M., Futaki, S., Gariboldi, M., Georgii-Heminger, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jaki, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, H., Kollas, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morita, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakanishi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okasaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavoni, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sadelain, A., Schneider, C., Schombach, C., Sekiguchi, K., Sempke, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Spelling, S., Scuppa, E., Sugura, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamashita, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hilde, M., Bull, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Bruscia, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Kono, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Wachihi, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.

PANTOM Consortium

The transcriptional landscape of the mammalian genome

Science 309 (5740), 1559-1563 (2005)

16141072

AUTHORS
Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yag, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batilov, S., Engstrom, P.G., Mizuno, Y., Faghini, M.A., Sadelain, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.

CONSRM
Riken Genome Exploration Research Group

TITLE
Antisense transcription in the mammalian transcriptome

JOURNAL
Science 309 (5740), 1564-1566 (2005)

PUBMED
16141073

AUTHORS
(bases 1 to 2550)
Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Kono, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Wachihi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
Direct Submission

JOURNAL
Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.riken.jp).

COMMENT
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES
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Query Match
Best Local Similarity 55.8%; Score 1537.4; DB 6; Length 2550;
Pred. No. 0;
Matches 1877; Conservative 0; Mismatches 566; Indels 0; Gaps 0;

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DB 55 AGAGCTTGATCCAGTAAAGTCTGTGAAGAAAGTAAAGTCCCTCGGATAGCCTC 114
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Db 1855 CCAGTGTCTGTGATGATGATCTGTGCTGACTGTACCAATCGGGGCCATATCTGTGTCTG 1914
Qy 1861 GCTGTGACTGTGACCTCCCTCTGCAATTAATTTGATCTGAGTATCTGAGATGCTG 1920
Db 1915 GCTGTGACTGTGGGCTTCTCTGTCTTAATCTTGAACCTGCGCTGTATGTAGATGCTG 1974
Qy 1921 TGCCAGTGAACCCAGACTCGGCGCAGGGCCAGSAAATATACCTTTAGAAACTCCAAAGA 1980
Db 1975 TGTCAATGACACAGAACAGGCAACAGGCGCAGGCAATCCCTTTAGAGAACTCCAGAGA 2034
Qy 1981 AACCTTCAAGTTTCAATGCTTTTATTTCAATATGTAACATGATTTCTGCTGGGTGAAGT 2040
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Qy 2041 GAATTTGATCTTACTTGAAGAAAGAAATATACGATTTTGTCTTCAAGAGAGAACTTT 2100
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Qy 2161 ATCTTTGTTTGTCTCCCACTTTGTCCAGATGAGTGTGCTTATGAACTTATTTT 2220
Db 2215 ATCTTTGCTGTGTCTCCCACTTTCATCCAGATGAGTGTGCTTATGAACTTATTTT 2274
Qy 2221 GCCCATACAAATCTCTTTCAATGAGAGATCTAATTAATCTTACTTACTGAAACC 2280
Db 2275 GCCCATCAATATCTTCTCAATGAAAGCTGTGATTAATCTTACTTGTGTGAAACC 2334


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Db      1261 GACAGACATGCGCTGGGCTGAGAGCAATATGTTGTTGAAATTTGTCGATATGCTT 1320
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Db      1331 ACAGGCTGCTTTCAGATGCTTACCTCCAGAGTCAAGGTCTTGAACCTTACAACANC 1380
Oy      1447 AAAATTAAGAGCGTTCCTAAACAGTCGTAAAAGTGAAGCTTTGCAAGATCAATGTT 1506
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Oy      1507 GCTTTCATTTCTTAACTGACCTTCTGATGTGCGACCTTTAGACAGCTTTCTGATATG 1566
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Oy      1867 ACTGTGACCTCCCTCTGTGACTTACTTGTGATTCCTGCTGTATCTCAGATGCTGTG 1926
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Oy      1927 TGGACCCAGACTCGGGCGAGGGCGAGGAACATACCTTGAAGAACTCCAAAGAAAC 1986
Db      1861 TGGACACAGACCAAGGACAGGGCCAGGCAATCCCTTTAGAGAACTCCAGAGAAAC 1920
Oy      1987 CAGTTTCATGCTTTTATTTATTAATGATGAACATGATTTGCTGCTGGGTGAAAAGTGA 2046
Db      1921 CAGTTCATGCTTTTGTCTCTCAATAGTGAATGATTTCTGCTGGGTGAAAAGTGA 1980
Oy      2047 GTACTTACCTTGAAGAAAGATATATACGATTTGCTTCTCATGAGAGAACTTTGTCC 2106
Db      1981 CTATCCCACTTGAAGAAAGATGCAATCCGGGTTTGCTCCATGAGAGAACTTTGTCC 2040
Oy      2107 GGCAGAGAGATTTGGAAGAAATATCATCACTGATGAGAGAGTGAAGTCAAGTCACTT 2166
Db      2041 GGCAGAGAGATTTGGAAGAAATATCATCACTTCAATGAGAGAGTGAAGTCAAGTCA 2100
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Oy      2227 CACATCTCTTTCATGAGAGATTAATTAATTAATCTTCACTTATGTAAGCACTTCA 2286
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RESULT 5 AK154253 LOCUS DEFINITION

AK154253 2522 bp mRNA linear HTC 21-SEP-2005
Mus musculus NOD-derived CD1c +ve dendritic cells cDNA, RIKEN
full-length enriched library, clone: F630012E11 product: coll-1-like
receptor 6, full insert sequence.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AK154253 1 GI:74178406
HTC, CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

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Direct Submission
Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome-gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site for further details.
URL: http://genome-gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

FEATURES

source
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/cell_type="NOD-derived CD11c +ve dendritic cells"
/clone_jib="RIKEN full-length enriched mouse cDNA library"
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misc-feature
/note="putative
coll-like receptor 6 (MGI:1341296 GB|BC055366,
evidence: BLASTN, 99%, match=2490)"

ORIGIN

Query Match 55.4%; Score 1525.4; DB 6; Length 2522;
Best Local Similarity 76.8%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 566; Indels 1; Gaps 1;

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27 GAGCTTGATCCAAATTAATTCCTGTAAGATGTAAGTCCCTCGGATACCTCT 86
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62 ACATCATGACCAAGACCAAGAACTATGTTAAAGCTTCATTTGTCCTATGA 121
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87 GCAACATGAGCCAAAGACGAAAGAACCATGCGGGAGTTCCACTTTGTCGCCCTGG 146
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OY	302	CAGTTTGGACCTTCCCATAGACGAATCCAGCTACTGATTTAAAGTTTCAAGTTCA	364
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OY	362	ACCGAGATTATGGAATATTTGGATTATCTCATTAATGAGTGCMAAAGATATCCGCCATC	421
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Db	507	GTAAGGAATTTGGCACTTATCACAACATGAAATTTCTGGGATTAAGTGTCTAAGCTGC	566
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OY	842	TGAAAGCACTTGGAAATGCTGTGTCAGAGTCTTCAATTTCTTTGGCCCAACCTGTGG	901
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Db	1347	GCAATATACAGAAACATGCGCTGGGCTCAGAGCATATTTGTGTGAATTTTGTCTTCGAT	1406
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Db	1947	TGTCAAGTGAACAGACCAAGCAAGGCCAGAGGCCACATCCCTTAAAGAGAACTCCAGAGA	2006
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Db	1955	AGTTATAGAGGAAGCCCACTAAGAGACTTTCAACTGTCTGAATTAATCTCTGCAACATTAAT	2014
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DEFINITION	001212BPMAM001548FL BPMA Bos taurus cDNA, mRNA sequence.		
ACCESSION	DY109015		
VERSION	DY109015.1	GI:86272292	
KEYWORDS	EST.		
SOURCE	Bos taurus (cattle)		
ORGANISM	Bos taurus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.		
AUTHORS	1 (bases 1 to 3051) McClulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S., Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T., Hagemann,L., Lee,R., Hein,M., Johnstone,P., Magdool,N., McMahon,C., McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J., Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J., Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and Atkinson,P.		
TITLE	AgResearch, Genesis and Primary Industry Victoria Bovine EST project		
JOURNAL	Unpublished (2006)		
COMMENT	Contact: Magdool N AgResearch Ltd. Invermay Agricultural Centre, Puddle Alley, Private Bag 50034, Mosgiel, New Zealand Email: nauman.magdool@agresearch.co.nz.		
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QY	358	TTCAACCGAATTTAGATATTTTGATTTATCTCATATCAAGTTCGAAAGATATCCGCG	417
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KEYWORDS
Htc; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
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AUTHORS
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
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10349636

REFERENCE
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AUTHORS
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JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
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AUTHORS
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)
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11076861

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AUTHORS
RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
JOURNAL
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PUBMED
Nature 409 (6821), 685-690 (2001)
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AUTHORS
FANTOM Consortium
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The transcriptional landscape of the mammalian genome
PUBMED
Science 309 (5740), 1559-1563 (2005)
PUBMED
16141072

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7 Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yag, C. C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K. C., Hallinan, J., Matlack, J., Hume, D. A., Lipovich, L., Batalov, S., Engstrom, P. G., Mizuno, Y., Feghli, M. A., Sandelin, A., Chalk, A. M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.
AUTHORS
RIKEN Genome Exploration Research Group
JOURNAL
Antisense transcription in the mammalian transcriptome
PUBMED
Science 309 (5740), 1564-1566 (2005)
PUBMED
16141073

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Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Kono, H., Murata, M., Nakamura, M., Ninomiya, N.,

TITLE
JOURNAL

Nishiiori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shiba, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watabiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse cDNAs.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://phantom.gsc.riken.jp/.
Location/Qualifiers

FEATURES

source

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Tel: 82 31 290 1593
Fax: 82 31 290 1792
Email: dhyoon@rda.g

FEATURES
source

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Db 27 GAAGATTAGTCCCTCAAGCGGGGACAATCCATTCCATGTTCCTGTGAGCTAAGAGA 86

1683 ATTTGTCAAATATAGACCAAGTATCAAGTGAAGTGTAGAGGGCTGGCCTGATTCTTA 1742

Db 87 CTTCA^{TC}CAAGTATAGGCCAAGTATCAAGTGACGTGGTAGAGGGCTGGCC^{TC}TGAGTCTTA 146

1743 TAAGTGTACTACCCAGAA GTTATAGAGGAAGCCCACTAAAGGACTTTCACATGCTGA 1802

Db 147 TAAGTGTACTATCCGGAAGCTACAAGGAGGCCCTCGGAGGACTTCCAGGTATCTGA 206

1803 ATTATCCTGCACATACTCTGCTGATCGTCACCATCGGTGCCACCATGCTGGTGTGGC 1862

Db 207 GCTATCCTGCAACACAGCTCTGCTGATCGTCACCATGTGTGTCCTGGGCTGGTGTGGC 266

1863 TGTGACTGTGACCTCCCTCTGCATCTACTTGGATCTGCCCTGGTATCTCAGGATGGTGTG 1922

Db 267 TGTGCTGTGACTGTCCCTCTGTATCTACCTGGATCTGCCCTGGTACCTCAGGATGGTGTG 326

QY 1923 CCAGTGGACCCAGACTCGGGCGAGGGCCAGGAACATACCCCTTAGAAGACCTCCAAGAA 1982

Db 327 TCAGTGGACCCAGACCCGGCGCAGGCCAGGAATGTACCCCTTGGAGAAGACTCCAAGAAC 386

1983 CCTCCAGTTTCATGCTTTATTCATATAGTGAACATGATTCGCCCTGGTGAAGAAGTGA 2042

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Db 447 ATTATACCTAACCTAGAAAAAGAGATATTAAGATTTCCTCCATGAGAGAACTTCG 506

2103 CCCTGGCAAGGCAATTGTGAAATATCATCACTGGCAATTGAGAAGAGTTACAAGTCCA: 2162

Db 507 TGCTGGCAGAGCATTTGTGAAATATCATCAACTTGCATTGAGAAAGTTACAAATCCAT 566

2163 CTTTGTTTGTCTCCCACTTTGTCCAGAGTGAGTGGTGGCCATTCGAACTCTATTTTGC 222

Db 567 CTTGTCTTGTCTCCCACTTTGTCCAGAGCGAATGGTCCATTATGAACCTACCTTTC 626

2223 CCATCACAATCTTTCAATGAAGGATCTAATACTTAATCCCTCAATCTTAATGGAACTCAAT 2282

Db 627 CCACCACATCTCTCCATGAGGATCTGATACCTAACTCCATGATCTTGGATCCCAT 886

2283 TCCACAGACAGCATTTCCCAACAGTACCACACAGCTGAAGGCTCTCATGACGCAGCGAC 2342

D5 687 TCCACAGTATTCATTCTAGCAGCTACCCACAGCTAAGAGCTCTCATGGCACAAGAAC / 46

2343 TTATTGCAGTGGCCCAAGGAGAAAGCAACGTGGGCTCTTTGGCTAACATAGAGC 2401

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QY 2403 CGCTTTAATATGAATTAA 2422
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 LOCUS DA673961 NEMRP2 Homo sapiens cDNA clone NEMRP2004649 5', mRNA
 DEFINITION sequence.
 ACCESSION DA673961 GI:80920622
 VERSION DA673961.1
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 573)
 Kimura, K., Wakematsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)
 16344560

JOURNAL DB143901 564 bp mRNA linear EST 10-DEC-2005
 PUBMED DB143901 THYMU3 Homo sapiens cDNA clone THYMU3018225 5', mRNA
 COMMENT sequence.
 ACCESSION DB143901
 VERSION DB143901.1 GI:83521199
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Homnidae; Homo.
 1 (bases 1 to 564)
 Kimura, K., Wakematsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)
 16344560

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 Best Local Similarity 99.8%; Pred. No. 4.1e-130;
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QY 461 ATTTCAGAGCCCTGCCATCTGTAAAGATTGGCAACTTATCACAAGTGAATTTCTTGG 520
 Db 1 ATTTCAGAGCCCTGCCATCTGTAAAGATTGGCAACTTATCACAAGTGAATTTCTTGG 60

QY 521 GATTGAGTGCTATGAAGCTGCAAAAATTGATTTGCTGCCAATTGCTCATTGTCATCTTA 580
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QY 641 AAATTCTGAATGCAAAACCCCTTCACCTTGTCTTTTTCACCCCACTAGTTATTCGCTATCC 700
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QY 701 AAGTGACATATCAGTTAATACCTTTAGGGTGCTTACAGCTATATATTAATTGAATG 760
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QY 1001 TCACGACCAAGTCTTTCTGTTTTCACAGACAG 1033
 Db 541 TCACGACCAAGTCTTTCTGTTTTCACAGACAG 573

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 VERSION DB143901.1 GI:83521199
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 564)
 Kimura, K., Wakematsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
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 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)
 16344560

JOURNAL DB143901 564 bp mRNA linear EST 10-DEC-2005
 PUBMED DB143901 THYMU3 Homo sapiens cDNA clone THYMU3018225 5', mRNA
 COMMENT sequence.
 ACCESSION DB143901
 VERSION DB143901.1 GI:83521199
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 564)
 Kimura, K., Wakematsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
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 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
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 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
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 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)
 16344560

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 DB 1 CATATAGTGAACATGATTCCTGCTGGGTGAAAAGTGAATGGTACCTTAGAAAAAG 60

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QY 2126 ATATCATCAACGTCATGAGAAAGTTACATCCATCTTTTGTGCTCCCACTTTG 2185
 DB 121 ATATCATCAACGTCATGAGAAAGTTACATCCATCTTTTGTGCTCCCACTTTG 180

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 DB 181 TCCAGAGTGAAGTGTGCTCATTAAGAACTGTATTTTGGCCCATCAATCTCTTTCATGAA 240

QY 2246 GATCTAATTAACCTTAATCCCTCATCTTACTCTGAAACCATTCACAGAAAGACATTTCCCA 2305
 DB 241 GATCTAATTAACCTTAATCCCTCATCTTACTCTGAAACCATTCACAGAAAGACATTTCCCA 300

QY 2306 AGTACCAACAGCTGAAGGCTCTCATGACGACGAGCTTAATTGGCAGTGGCCCAAGAGA 2365
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QY 2366 AAAGCAAAAGTGGGCTCTTTTGGGCTAAACATTAGAAGCGCTTTTAATAGAAATTAAC 2425
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 DEFINITION sequence.
 ACCESSION DA619469
 VERSION DA619469.1 GI:80859889
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 SOURCE Homo sapiens (human)
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 609)

REFERENCE
 AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
 Yamashita,R., Yamamoto,J., Sekine,M., Tsuritan,K., Wakaguri,H.,
 Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
 Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
 Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
 Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes

TITLE JOURNAL
 PUBMED Genome Res. 16 (1), 55-65 (2006)
 COMMENT 1634360
 Contact: Takao Isogai

FLU Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction:
 Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3'-end one
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QY 122 TCATTAATGTTGGAACCGAATTCAGTCTCCGACGAAAGAAATTTGCACTAGCAAGT 181
 DB 177 TCATTAATGTTGGAACCGAATTCAGTCTCCGACGAAAGAAATTTGCACTAGCAAGT 236

QY 182 CAAAAAGAGTCTTATTCATGTTCCAAAAGACATACGCTGAAAAACCAAGCTTAGATA 241
 DB 237 CAAAAAGAGTCTTATTCATGTTCCAAAAGACATACGCTGAAAAACCAAGCTTAGATA 296

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 DB 297 TGTCTCAGAACTACATCGCTGAGCTTCAGGTCTGTGACATGAGCTTTCTATCAGATTGA 356

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QY 422 CTATTGTAGATTTCAGGACATTTAAGTCTCTCATTCATGATTTCAAGGCTCCCATCT 481
 DB 477 CTATTGTAGATTTCAGGACATTTAAGTCTCTCATTCATGATTTCAAGGCTCCCATCT 536

QY 482 GTAAGAAATTTGGCACTTATCAACAATGATTTCTTGGGATGAGTGTCTAAGAGCTGC 541
 DB 537 GTAAGAAATTTGGCACTTATCAACAATGATTTCTTGGGATGAGTGTCTAAGAGCTGC 596

QY 542 AAAAATTGATTT 554
 DB 597 AAAAATTGATTT 609

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 DEFINITION 602831164r1 NCI_CGAP_C024 Mus musculus cDNA clone IMAGE:4986086 5',
 mRNA sequence.

ACCESSION BG963497
 VERSION BG963497.1 GI:14351134
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
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 REFERENCE NIH-MGC http://mgi.nci.nih.gov/1 (bases 1 to 772)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabrs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
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 QY 1955 ACATACCTCTAGAGAACTCCCAAGAACTTCAGATTTATGCTTTATTTATATATAGTG 2014
 DB 421 ACATCCCTTAGAGAACTCCAGAGAACTTCAGATTTATGCTTTATGCTATACAGTG 480

QY 2015 AACATGATTCGCTGGGTGAAAGGAAATGGTACTTACCTAGAAAAAGAGATATAC 2074
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 QY 2254 AACTTAATCTTCATCTTACTGGAACTTCAGAACTTCAGAACTTCAGAACTTCAGAA 2306
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RESULT 14
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 sequence.
 ACCESSION CK980631
 VERSION CK980631.1 GI:45498611
 KEYWORDS EST.
 SOURCE Bos taurus (cattle)
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REFERENCE 1 (bases 1 to 698)
 Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasparre, L.C.
 Production of EST from CDNA libraries derived from immunologically activated bovine gut
 Unpublished (2004)
 TITLE Contact: Tad S. Sonstegard
 JOURNAL Bovine Functional Genomics Laboratory
 COMMENT Animal and Natural Resources Institute
 Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
 Tel: 3015048416
 Fax: 3015048414
 Email: tads@anri.barc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred
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 by cross_match using options -mismatch 12 -minscore 12
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Fri Jun 9 14:07:32 2006

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